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Sent: To:

Helmer, Georgia Monday, July 29, 2002 10:59 AM STIC-Biotech/ChemLib

Subject:

09/643,755

Could you please do sequence searches of SEQ ID 1, 2, and 3 of this case, 09/643,755.

SEQ ID 1 and 3 are DNA. SEQ ID 2 is protein.

Could you also do an oligo search of SEQ ID 1 and 3.

The commercial and inhouse databases.

Thanks in advance for you assistance.

Georgia L. Helmer Ph.D. Patent Examiner Crystal Mall 1, 9D14 **AÚ 1638** 703-308-7023 Georgia.Helmer@USPTO.gov mailbox 9e12

GMMS G1.

Point of Contact: Toby Port Technical Info. Specialist CM1 6A04 703-308-3534

Searcher: Phone: ____ Location: _ Date Picked Up: _ Date Completed: __ Searcher Prep/Review: __/__ Clerical: Online time: ___

TYPE OF SEARCH: NA Sequences: ____ AA Sequences: _____/ Structures: ____ Bibliographic: _____ Litigation: _____ Full text: Patent Family: _______ Other: _____

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ALIGNMENTS

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/organism="Bos taurus" /odb_xref="taxon:9913" 1. 1173 /note="unnamed protein product"	11173	Location/Qualifiers	SemBioSys Genetics Inc. (CA)	Patent: WO 0114571-A 1 01-MAR-2001;	Commercial production of chymosin in plants	van Rooijen, G., Keon, R.G., Boothe, J. and Shen, Y.	1 (bases 1 to 1173)	Bovidae; Bovinae; Bos.	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Bos taurus	COW.		AX088019.1 GI:13396947	AX088019	Sequence 1 from Patent WO0114571.	AX088019 1173 bp DNA linear PAT 17-MAR-2001		

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J00003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harris,T.J.R., Lowe,P.A., Lyons,A., Thomas,P.G., Millican,T.A., Patel,T.P., Bose,C.C., Carey,N.H. molecular cloning and nucleotide sequence of cdn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              been identified as coding for preprochymosin b. sequence comparison indicates that the precursors for chymosins a and b differ by only two amino acids, and for b and c by only four amino acids.
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bovine (calf) cdna
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nilarity 87.8%;
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20. 73
/note="presequence"
200. 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAA30448.1"
/db_xref="GI:162860"
/db_xref="GI:162860"
/translation="MRCLVVLLAVFALSQGAEITRIPLYKGKSLRKALKEHGLLEDFL
QKQQYGISSKYSGFGEVASVPLTNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDEWVPS
IYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYGTGSMQGILGYDTVTVSNIVDIQQT
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/db_xref="taxon:9913"
<1. .1305</pre>
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1. .1305
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/codon_start=1
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26. .1171
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Cetartiodactyla;
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Pred. No. 5e-263;
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actyla; Ruminantia;
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. and Doel, M.T.
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Unknown.
Unclassified.
1 (bases 1 to
Kato, E.K. and
                           AR002347
Sequence 2 :
AR002347
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Stuart, W. Dorsey
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                           AGGCCATCCTGGACACGGGCACCTCCAAGCTGGTCGGGCCCAGCAGCGACATCCTCAACA
                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity
980; Conserv
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hilarity 87.7%;
Conservative
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374 c 339 g
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Location/Qualifiers
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Pred. No. 4.7e-262;
0; Mismatches 138;
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Query Match Best Local :

76.5**%**; 87.7**%**;

Length

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                         cctccgcctataccagccaggatcaagggttctgcaccagtggattccagagtgagaacc
                                                                                                                                                                                                                                                                                   TCCAGCAGGCCATTGGAGCCACACAGAACCAGTACGGTGAGTTTGACATCGACTGCGACA
                                                                                                                                                                                                                                                                                                                      ttcagcaagctattggagccacacagaaccagtacggtgagtttgacatagattgcgaca
activity
Patent: F
                                                                                                                                                   Sequence
104058
104058.1
                                                                                                       Unclassified.

1 (bases 1 to 1175)
Cashion,L.M., McCaman,M.T., Rice,C.W. and Recombinant DNA coding for a polypeptide of
                                                                                                                                  Unknown
                                                                                                                                        Unknown
                                                                                                                                                                       I04058
                                 Similarity
                          Conservative
                                                                  а
                                                                                          EP 0123928-A2 5 07-NOV-1984;
                                                                                                                                                                  Çī
                                                                             Location/Qualifiers
1. .1175
                                                                 /organism="unknown"
356 c 318 g
                                                                                                                                                                  from
                                76.4%;
87.6%;
                                                                                                                                                                 Patent
                          Score 895.6; DB 6;
Pred. No. 1.4e-261;
0; Mismatches 139;
                                                                                                                                                                  1175
EP 013
                                                                                                                                                                 175 bp
0123928.
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displaying
                                       Length
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                           Indels
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cctccgcctataccagccaggatcaagggttctgcaccagtggattccagagtgagaacc
                                                                              tyttctcggtttacatggacaggaatggccaggagagcatgctcacgcttggagctattg
                                                                                                                                             cagagtactcgatacctgtgtttgacaacatgatgaaccgacacctagtagctcaagact
                                                                                                                                                                            accttagctacatgcctacagttgtctttgagatcaacggcaagatgtacccactgaccc
                                                                   ttcagcaagctattggagccacacagaaccagtacggtgagtttgacatagattgcgaca
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BASE COUNT
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AUTHORS
TITLE
JOURNAL
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Local (
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Unclassified.

1 (bases 1 to 2733)

1 (bases 1 to 2733)

Moloney,M.M.

Preparation of heterologous proteins on preparation of heterologous proteins on Location/Qualifiers

1. 2733

--nismm*"unknown**

689 t
tttgacaacatgatgaaccgacacctagtagctcaagacttgttctcggtttacatggac
                                                                                                          ttcgatggcatccttggtatggcatacccatcgctcgcgtcagagtactcgatacctgtg
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Sequence 6
AR073077
AR073077.1
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Unknown.
Unclassifi
                                                                                                                                                                                                                                                                                                                               Similarity 88.471; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from
                                                                                                                                                                                                                                                                                                                                       76.3%;
88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    patent
                                                                                                                                                                                                                                                                                                                               Score 894.8;
Pred. No. 2.7e
0; Mismatches
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5948682
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2.7e-261;
ches 127;
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AUTHORS
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MEDLINE
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 sig_peptide
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bovine chy
J00002
                                                                                                                                                                                                                             chymosin (rennin) is the major proteolytic enzyme in the fourth stomach of the unweaned calf. two chromatographically distinct forms are known and a third seems likely (see bovchymob and bovchymo), this sequence has been tentatively identified as chymosin a; it differs from chymosin b by only two amino acids from chymosin c by another amino acid. [1] argues that the
                                                                                                                                                                                                                                                                                                                                                                                                         J00002.1 GI:162857
chymosin; chymosin A; rennin.
bovine (calf) cdna of fourth s
Bos taurus
Busaryota; Metazoa; Chordata;
Bukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                          molecular cloning and characterization coding for bovine chymosin
                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinae; Bos.

1 (bases 1 to 1275)

Moir,D., Mao,J.I., Schumm,J.W.,
Taunton-Rigby,A.
                                                                                                                                                                                                                    different chymosins
                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chymosin a (rennin) mrna
                                                                                                                                                                                                                                                                                                                , 127-138
VGLSTQEPGDVFTYAEFDĞİLGMAYPSLASEYSIPVFDNMMNRHLVAQDLFSVYMDRN GQESMLTLGAIDFCYYTGSLHRVPVTVQQYWQFTVDSVTISGVVVACEGGCQAILDTG TSKLVGPSSDILNIQQAIGATQNQYDEFDIDCDNLSYMPTVVFEINGKMYPLTPSAYT SQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDRANNLVGLAKAI"
                                                           /codon_start=1
/protein_id="Aa30447.1"
/protein_id="Aa30447.1"
/db_xref="GI:162858"
/translation="MRCLVVLLAVFALSQGAETTRIPLYKGKSLRKALKEHGLLEDFL
/translation="MRCLVVLLAVFALSQGAETTRIPDETVLFDTGSSDFWVPS
IYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYGTGSMQGILGYDTVTVSNILDIQQT
                                                                                                                                                                                                         gene
                                                                                                                                                       /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                 /note="preprochymosin
                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2727
                                                                                                                                                                                                                                                                                                                (1982)
                                                                                                                                                                                                                 are probably polymorphic
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                                                                                                                                                                                                                                                                                                                                                                                                                                   rennin.
fourth stomach
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actyla; Ruminantia; Pecora;
                                                                                                                                  a<sub>n</sub>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
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                                                                                                                                                                                                                                                                                           fourth
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   accttagctacatgcctacagttgtcttttgagatcaacggcaagatgtacccactgaccc
                                                 ttcagcaagctattggagccacacagaaccagtacggtgagtttgacatagattgcgaca
                                       TCCAGCAGGCCATTGGAGCCACACAGAACCAGTACGATGAGTTTGACATCGACTGCGACA
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978; Conservative
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87.5%;
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tcgttgctgttactcacgctgctgagatcacccgcattcctctctacaaaggtaagtctc
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                                                  tgttctcggtttacatggacaggaatggccaggagagcatgctcacgcttggagctattg
                                                                                                                                                                                                                                                                atgtetteaectatgeagaattegatggeateettggtatggeataeceategetegegt
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atccatcctactacacaggatctcttcactgggttccagtcactgtgcagcagtactggc
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CDNA encoding chymosis

E00075

E00075.1 GI:2168379

JP 1983009687-A/1.

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Nooman, H.K., Maikeru, T.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
                                                                                 ø
                                                                                                     /product='pre-pro-chymosin'
1.ocation/Qualifiers
1.1290
                                                                                /organism="Bos taurus"
/db_xref="taxon:9913"
384 c 334 g
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Eutheria; Cetartiodactyla; Ruminantia; Pecora;
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                                            attcccagaaatggatcttgggagatgtgttcattcgtgagtactacagcgtctttgaca
                                                                     aattcactgtggacagtgtcaccatcagcggtgtggttgttgcatgtgaaggtggatgtc
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gcaagaaccaccaaagattcgatccgagaaagtcgtccaccttccagaacttaggcaaac
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1 (bases 1 to 1291)
Carey,N.H., Doel,M.T., Harris,T.J.R.,
A process for the production of a poly
Patent: EP 0068691-A 29 05-JAN-1983;
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/protein_id="CAA01244.1"
/protein_id="CAA01244.1"
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VGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSIPVFDNMMNRHLVAQDLFSVYMDRI
GQESMLTIGAINFSYYTGSLHWVPUTVQQYWDFTVDSTYIGSCVAALDTG
TSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYMPTUVFEINGKMYPLTPSAYT
SQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDRANNLVGLAKAI"
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/db_xref="taxon:32630"
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                                                                                                                            cDNA encoding bovin
E00144
E00144.1 GI:216844
JP 1984021392-A/1.
Patent: JP 1984021392-A 1 03-FEB-1984;

GENEX CORP
OS bovine calf
S bovine calf
PN JP 1984021392-A/1
PN J9 1984021392-A/1
PP 30-FEB-1984
PF 30-JUN-1983 JP 1983119481
PR 01-JUL-1982 US 82 394433, 13-APR-1983 US 83
CHIVAARUSU EI BASUBETSUTO
PC C12N15/00,C07H21/04,C12N1/20,C12P19/34,C12P21/02,(PC C12R1:19);
                                                                           CATTLE KIMOCIN
                                                                                              unclassified.
1 (bases 1 to 1289)
                                                                                                             unidentified. unidentified
                                                                                                                                    GI:2168443
                                                                                                                                                    bovine
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aattcactgtggacagtgtcaccatcagcggtgtggttgttgcatgtgaaggtggatgtc
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                                                                                     tgttctcggtttacatggacaggaatggccaggagagagcatgctcacgcttggagctattg
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                                                                                                                                                                                                                                                                                                     GCAAAAACCACCAGCGCTTCGACCCGAGAAAGTCGTCCACCTTCCAGAACCTGGGCAAGC
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hypothetical: No;
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Location/Qualifiers
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/db_xref="taxon:32644"
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87.48;
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Pred. No. 9e-261;
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/product='bovine
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Local Similarity 87.5%;
hes 977; Conservative
         cctccgcctataccagccaggatcaagggttctgcaccagtggattccagagtgagaacc
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                                                                           CATCAGCAGCAAGTACTCCGGCTTCGGGGAGGTGGCCAGCGTCCCCCTGACCAACTACCT
                                                                                     catcagcagcaagtactccggcttcggtgaagttgctagcgtgccacttaccaactacct
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                                     GGACAGTCAGTACTTTGGGAAGATCTACCTCGGGACCCCGGCCCCAGGAGTTCACCGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                           I08097
Sequence
I08097
                                                                                                                                                                                                                                                                                           1 (bases 1 to 2726)
van den Berg, J.A.D. and Brake, A.J.D.
DNA constructs containing a Kluyveromyces
sequence for directing secretion of hetero
Patent: EP 0301669-A1 5 01-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                      Unknown
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Pred. No. 9.5e-261;
0; Mismatches 140;
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                                                                                DNA coding of prepries to 100108 E00108 GI:216840 JP 1983109499-A/1. unidentified
RECOMBINED DNA
Patent: JP 1983109499-A 1
UNILEVER NV
OS calf
                                               Yan
                                                         unclassified.
1 (bases 1 to 1311)
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                                                                                                                                           coding of prepro chymosin
                                               Koruneerisu, S.B.,
                                                                                                                     GI:2168409
                          29-JUN-1983;
                                               Adorianusu, M.R.
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PD 29-JUN-1983
PF 14-OCT-1982 JP 1982180549
PR 14-OCT-1981 GB 81 8131004
PI YAN MAATO, KORUNEERISU SEDDORUSU BERURITSUPUSU, PI ADORIANUSU MARINUSU REDEBOERU, RUTSUPO EDENSU PC CO7H21/04,C12M120,C12M15/00//C12P21/00;
CC strandedness: Double;
CC topology: Linear;
CC topology: Linear;
CC anti-sense: No;
CC *source: tissue_type=stomach;
FH Key Location/Qualifiers
FH Key Location/Qualifiers
FT sig_peptide 24..1169
FT sig_peptide 72..1166
FT mat_peptide 72..1166
FT mat_peptide 72..1166
FT mat_peptide 198..1166
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/db_xref="taxon:32644"
397 c 338 g 26
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Pred. No. 1.4e-260;
0; Mismatches 141;
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Debuitsudo, B., Ronarudo, U.D., Jierarudo, R.F., Arison, T.R.,
Robanto, J.N., Jien, I.M., Donarudo, T.M. and Kurisutofuaa, G.G..
USE OF GAL YEAST PROMOTOR

Patent: JP 1985058077-A 3 04-APR-1985;
KORABORATEBU RES INC
OS Bovine
PN JP 1985058077-A/3
PI 1985058077-A/3
PP 28-FEB-1984 JP 1984035472
PR 28-FEB-1984 US 83 470911
PI DEBUTSUDO BOTSUTOSUTEIN, RONARUDO UEIN DEIBUISU, PI
JIERARUDO RARUFU FUNKU,
PI ARISON TAUNTON RIGUBII, ROBAATO JIENTORII NOURUTON, JIEN I
MAO, PI DONARUDO TEIRAA MOA, KURISUTOFUAA GOTSUDOFURII GOFU PC
C12N15/00, C07H21/04, C07K13/00, C12N1/16, C12P21/02, (C12N1/16, PC
C12R1:865);
PC (C12P21/02, C12R1:865);
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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JP 1985058077-A/3.
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*source: clone=293-207 & 293-118/37;
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Location/Qualiflers
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87.48;
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253. .1347
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205. .1347
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Pred. No. 1.4e-260;
0; Mismatches 141;
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Search completed: July 31, 2002, 18:18:54 Job time: 20085 sec

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Maximum Match 100%
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Perfect score:
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Maximum DB seq length: 2000000000
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ALIGNMENTS

RESULT AAS00569 Bovine pre-pro-chymosin DNA sequence. 14-MAY-2001 AAS00569 standard; DNA; 1173 BP (first entry)

Chymosin; transcription regulator; terminator sequence; soybean; corn; pre-pro-chymosin; rape seed; sunflower; cotton; tobacco; alfalfa; wheat; barley; oats; sorghum; Arabidopsis thaliana; potato; flax; linseed; rice safflower; oil palm; ground nut; Brazil nut; coconut; castor; coriander; squash; jojoba; ds. mat_peptide misc_feature CDS Bos sig_peptide qs. /note= "Pro s 202..1170 /*tag= d /product= ' /product= /*tag= 79..201 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Producing chymosin in seeds of plants such as rice, flax, rape seed, transforming plant cell with a nucleic acid encoding chymosin operable linked to transcription regulator and terminator sequences -
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pre-pro-chymosin; rape seed; sunflower; cotton; tobacco; alfalfa; wheat; barley; oats; sorghum; Arabidopsis thaliana; potato; flax; linseed; rice; safflower; oil palm; ground nut; Brazil nut; coconut; castor; coriander; squash; jojoba; ds; phaseolin; promoter; terminator; mutant: Franch haar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA fragment having region specific for lactic acid bacteria is contained in plasmid in microorganism used in prodn. of protein and food prodn. eg cheese.
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                                            cagagtactcgatacctgtgttttgacaacatgatgaaccgacacctagtagctcaagact
                                                                                          ctgtctccaacattgtggacattcaacagacagtaggacttagcacccaagaaccaggtg
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      nt DNA coding for milk clotting in transformed bacteria
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Best Local S
Matches 763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 897.2; DB 5;
Pred. No. 7e-273;
L7; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 U; 0 other;
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                      The DNA is that of a mammalian gene (open reading frame) encoding chymosin. The gene was placed in operable linkage with the al-3 promoter (see AAT03005). The al-3 gene controls the production of geranyl geranyl pyrophosphatase (GGPP) synthetase. GGPP is a precursor for carotenoids and xanthophylls. It has been shown that exposure to light increases the transcription level of GGPP synthetase 15-45 fold. Light activates a number of genes in the common bread mould, Neurospora. This can be used to regulate the expression of genes encoding heterlogous proteins, e.g. chymosin, in recombinant production systems. Use of a light-regulated promoter is a simple and effective way to control expression and allows timing to be adapted to the physiological status of the host.
                                                                                                                                                                                                               Nucleic
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gene; expression; control; chymosin;
B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reading frame
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274
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Query Match Best Local s Matches 980

Similarity

76.5%; 87.7%;

Score 897.2; | Pred. No. 7.2e 0; Mismatches

.2e-273;

Indels Length

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16-JAN-1981;
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/note= "CDS
850..1202
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1443..2733
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heterologous
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                                                B.napus plants.

CB.napus plants.

Chie DNA which encodes a chimeric fusion protein that consists of the coil-body targeting sequence, a transcription regulation sequence and the protein of interest can be used to produce antibodies, glycanases, hormones, proteases, protease inhibitors, seed storage proteins, thrombin inhibitors, hirudin, interleukins, chymosin, cysts cylanase, carp growth hormone, zein or a collagenase.

Che enzyme may be cleaved from the oil body protein or used in association with the oil body fraction.

Allows production by conventional systems. The expressed heterologous protein can be easily separated from host cell components due to the use of the oil body as a carrier protein.
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22-FEB-1991;
16-NOV-1993;
30-DEC-1994;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the nucleotide sequence of a HindIII fragment containing the oleosin-spacer-Met-prochymosin sequence. This HindIII fragment was joined to a nopaline synthase terminator and cloned into binary vector pCGN1559. The resulting plasmid was called pSBSOTPTNT and introduced into A.tumefaciens. The resulting bacterial strain was used to transform
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DB; AAY33830.
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91US-0659835.
93US-0142418.
94US-0366783.
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681 C;
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684 G;
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T; 0 other;
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                                                gatccgagaaagtcgtccaccttccagaacttaggcaaacccttgtctatacactacggt
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                                                                            gacttctgggtaccctctatctactgcaagagcaatgcctgcaaaaaccaccagcgcttc
                                                                                                                     aagatctacctcgggaccccgccccaggagttcaccgtgctgtttgacactggctcctct
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5.3e-272;
hes 127;
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RESULT ID AAQ14051
AAQ14051
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11-APR-1990;
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                                                                                                                   mammary
                                                                                                                             Prorennin; alpha-S1-casein
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                                                                                                                  gland;
                                                                                                                                                                                                        standard;
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           90DE-4012526
90DE-4011751
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                                                                                                                                                                                                        DNA;
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                                                                                                                            gene; insulin-like growth factor I;
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Recombinant DNA constructs for expressing protein in milk -contg. specific mammary gland transcription control region an signal sequence, providing high yield and easy prod. recovery
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                                                                                      Disclosure;
                                                                                                                                         1991-304858/42
                                                                                                                                                                          ) CONSORT ELEKTROCHEM
                                                                                      Page 21;
                                                                                     41pp; German.
                                                                                                              region and
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It was used as heterologous peptide/protein together with parts of the alpha-S1-casein gene in the produ. of DNA constructs. The heterologous peptide or protein may also be human insulin-like growth factor I. The constructs provide high yields of the protein with simple recovery from the milk. Activation of the gene occurs only in the mammary gland See also AAQ14050, AAQ14774-77.

Sequence 1210 BP; 278 Α; 356 C; 324 ر. ق 252 Η; 0 other;

Length

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nilarity 87.5%;
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Pred. No. 7.3e-272;
0; Mismatches 140;
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P-PSDB; AAP30446.
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                                                                                                                                                                                                                                DNA molecules comprising transform microorganisms prepro-enzyme and its all
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                                          ggggatgttttcatccgagagtattacagcgtctttgacagggccaacaacctggtgggg
                                                                                  gaccagggcttctgtaccagtggcttccagagtgaaaatcattcccagaaatggatcctg
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Search con Job time: completed: July me: 25748 sec 31, 21:11:57

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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BG937697 1Abo0SB01
A1326975 m]81e03.x
BG937723 1Abo0SD06
AK004109 Mus muscu
BG938086 1Abo11A08
AA028632 mil4c08.r
A1479358 tm27e07.x
A1324687 mil82b01.x
A1385490 mj81e03.y
AK00898 Mus muscu
AW86892 MRI-SN006
AK008886 Mus muscu
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BIB18940 603037434 AW959943 EST372014 BI762154 603049340 BF373812 MR2-SN000		BE840800 MR2-SN000 AW868711 MR1-SN006 BI821121 603035596 BI490133 603031966 RE841758 MR1-SN006	AA969042 op43d07.s W14201 ma99h09.r1 BF121716 601759230 W10274 ma37909.r1 BE841761 MR1-SN0006 AW863768 MR3-SN001	BE841740 MR1-SN006 AW867433 MR0-SN003 BE841714 MR1-SN006 BM069200 1d71a02.y BM053683 1d69b07.y	BE841742 MR1-SNOO6 BF299798 602030421 BF373831 MR3-SNOOO AW012992 SSERNOISK

ALIGNMENTS

source	FEATURES		REFERENCE AUTHORS TITLE JOURNAL COMMENT	KEYWORDS SOURCE ORGANISM	RESULT 1 BG938320 LOCUS DEFINITION ACCESSION VERSION
1472 // Organism="Bos taurus" //Ob xref="taxon:9913" //Clone_lib="Bovine Abomasum cDNA Library" /sex="Two males and one female mixed" /tissue_type="Gastrointestinal tissue (GIT)" /cell_type="Epithelial"	POLY PALIMETS FORWARD: M13 Forward BACKWARD: M13 Reverse Seq primer: T3 primer High quality sequence stop: 472 POLYA=NO. Location/Qualifiers	Dept of AFNS, University of Alberta 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada Tel: 780 492 0169 Fax: 780 492 4265 Email: smoore@afns.ualberta.ca The sequence best matches gb:BOVCHYMOA (bovine chymosin a (rennin) mrna) in main database at high score of 928.0 and E-value of 0.0	1 (bases 1 to 472) 1 (bases 1 to 472) Moore S.S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G. cDNA's from bovine abomasum tissue Unpublished (2001) Contact: Dr. Stephen Moore Boof Commics i aboratory	S E -	BG938320 472 bp mRNA linear EST 11-JUN-2001 lAbo15E12 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA sequence. BG938320 G1:14337692

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                                                                                                  1 (bases 1 to 631)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                                          Contact: Marra M/WashU-NCI Mouse EST Project Washington University School of Medicine Washington training Property School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis Tel: 314 286 1800
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                       AI892188 631 bp mRNA linear EST 15mj84c05.yl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:482792 5' similar to TR:Q28950 Q28950 PREPROCHYMOSIN
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                                                                                                                                               gctcgcgtcagagtactcgatacctgtgtttgacaacatgatgaaccgacccgacacctagtagc
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gtactggcaattcactgtggacagtgtcaccatcagcggtgtggttgttgcatgtgaagg
                                    agctattgatccatcctactacacaggatctctttcactgggttccagtcactgtgcagca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in correct orientation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 73.0
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Location/Qualifiers
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tggacagtgtcaccatcagcggtgtggttgttgcatgtgaaggtggatggtgaagctatct
                                                          actacacaggatctcttcactgggttccagtcactgtgcagtactggcaattcactg 784
                                                                                                                   CGATACCCGTGTTTGACAACATGATGAACAGGCACCTGGTGGCCCAAGACCTGTTCTCGG
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                                             ACTACAGAGGTCCCTGCACTGGGTGCCCGTGACAGTGCAGCAGTACTGGCAGTTCACTG
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BG937697.1
EST.
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Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA's from bovine abomasum tissue Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Smoore@afns.ualberta.ca
The sequence best matches gb:BOVCHYMOA (bovine chymosin a mrna)in main database at high score of 844.0 and E-value (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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1Abo05E01 Bovine
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FORWARD: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop:
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/lab_host="XL1-BlueMRF/-strain"
/note="Organ: Abomasum; Vector:
                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Bos taurus"
/db_xref="taxon:9913"
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                        MGI:293268
This clone was previously sequenced on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuo
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                            Possible reversed clone: similarity on High quality sequence stop: 446.
                                                                                                                                                                                                                                                                                                                                              data is from the
                                                                                                                                                                                                                                                                                                                                                                                          IMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston, R.
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        Dr. Minoru Ko (Wayne State University)
                                                                                                                                                                                                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
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Best Local Similarity 71.4
Matches 474; Conservative
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                                                                              sequence.
BG937723
BG937723.1
EST.
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
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1Abo05D06 Bovine
        1 (bases 1 to 399)
Moore, S.S., Hansen,
                                                            Bos taurus
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 Hansen, C., Li, C. bovine abomasum
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Contact: Dr. Stephen Moore
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: smoore@afns.ualberta.ca
The sequence best matches gb:BPU19786 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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High quality sequence
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/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
/lab_host="XLI-BlueNRF'-strain"
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ays embryo whole body cDNA, RIKEN full-length
clone:1110035E17:PEPSINOGEN F, full insert
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  prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGGGCCGCAACTCGAGTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA wen
                                                                                                cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                 Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/)
                                                                                                                                                                                                                                                                      Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC) RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoh Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409, 685-690 (2001)
5 (bases 1 to 1347)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                       further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                            cttggtatggcatacccatcgctcgcgtcagagtactcgatacctgtgtttgacaacatg
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                                              TGGCTACAAGGCCTCATCCCCCAGAATCTCTTTGCCTTCTACTTGAGCAGCAAGGATGAA
                                                                                                                                                CTGGGGCTGGGATACCCCAACCTTGGCCTTCAGGGAATCACACCCGTCTTTGACAACCTG
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XhoI. Host: SOLR.
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GTSLLTGPRSSIVNIQNLIGAKASGDGEYFLKCDTINTLPDIVFTIGSVTYPVPASAY
IRKDRSHNCRSNFEEGMDDPSDPEMWVLGDVFLRLYFTVFDRANNRIGLAPAA"
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/db_xref="G1:12835164"
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FGLSLEEPGIFMEYAVFDGILGLGYPNLGLQGITPVFDNLWLQGLIPQNLFAFYLSSK
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/db_xref="MGD:MGI:1900662"
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1 (bases 1 to 383)

Moore, S. S., Hansen, C., Li, C., CDNA's from bovine abomasum t CDNA's from bovine abomasum t Unpublished (2001)

Contact: Dr. Stephen Moore
. Beef Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                          sequence.
BG938086
BG938086.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                          BG938086
1AbollA08
                                                       Seq primer: T3 primer
High quality sequence
                                                                                                                 Email: smoore@afns.ualberta.ca
The sequence best matches gb:BPU19786
mRNA, complete cds) in main database a
E-value of 0.0
                                                                                                                                                               Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                COW.
                                                                               FORWARD: M13 Forward BACKWARD: M13 Reverse
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
                                                                                                                                                                                                                                                                                                                    Bos taurus
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/organism="Bos taurus"
/db_xref="taxon:9913"
                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
Contact: Marra W/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L4
                                                                                                                                                                                                Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Du
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 479)
              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                          The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 88...
38; Conservative
mouseest@watson.wustl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
111 c 113 g 76 t
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/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
/lab_Most="XL1-BlueMRF'-strain"
                                                                                                                                                                                                                                                                                                                                                                                                         GI:1494769
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Rodentia;
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                                                           Louis,
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                                                                                                                    GCTGCCCTGCCGTTCTGGACACAGGCACTGCGCTGTTGACGGGGCCTGGTAGAGACAT
                                                                                                                                                                       ATTGGCAGTTCACAGGACAGGATCACAATCAATGGTGAAGTGGTGGCTTGTCAAGGTG
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                                                                                                                                                                                                                                                                                              | aagacttgttctcggtttacatggacaggaatggccaggagagcatgctcacgcttggag
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                    AI479358 505 bp mRNA linear EST 14-itm27e07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE: 2157828 3' similar to TR: Q28950 Q28950 PREPROCHYMOSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.lln1.gov) for further information. MGI:277318
Possible reversed clone: similarity on wrong strand
            PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 444.
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Pred. No. 1e-63;
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AUTHORS
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                                                                                       cagaaatggatcttgggagatgtgttcattcgtgagtactacagcgtctttgacagggcc 1140
                                                                                                                                                        gcctataccagccaggatcaagggttctgcaccagtggattccagagtgagaaccattcc
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                                                                                                                                                                                                                                                                                                  caagctattggagccacacagaaccagtacggtgagtttgacatagattgcgacaacctt 960
AATAACCGTGTGGGGGCTGGCGAAGGCTGTCTGA
                                                                                                                                                                                                                                                                                 CAGGCCATTGGAGCCACTGCGGGCCAGTACAATGAGTTTGACATCGACTGCGGGCGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                           ACCCTTGNAAGTGTCATCATTGACGGCGTGGTGGTGGCCTGTGACGGTGGCTGTCAGGCC 446
                                                                                                                                      GCCTATACCAGCCAGGACCAGGGCTTTTGCACCAGTGGTTTCCAGGGTGACTATAGTTCC
                                                                                                                                                                                                            AGCAGCATTCCCACGGCTGTTTTTGAGATCCACGGCAAGAAGTACCCCCTGCCACCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further insert Length: 608 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 505)
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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EST.
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Location/Qualifiers
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE: 2157828"
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77.1%;
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Pred. No. 3.7e-60;
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426
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nes 343; Conserv
                              ggttgttgcatgtgaaggtggatgtcaagctatcttggataccggtacgtccaagctggt 869
                                                                                                                               tccagtcactgtgcagcagtactggcaattcactgtggacagtgtcaccatcagcggtgt 809
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AGTGGTGGCTTGTCAAGGTGGCTGCCCTGCCGTTCTGGACACAGGCAATGCCCTGTTGAC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
1 (bases 1 to 546)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:473065"
/clone_lib="Soares mouse p3NMF19.5"
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/db_xref="taxon:10090"
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Pred. No. 4.1e-59;
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B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                      MGI:293268
This read is a RESEQUENCE of a previously
This read has been verified (found to hit
                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                     Possible reversed
                                                                                                                                                                                                                                                                                                                     IMAGE Consortium (info@image.llnl.gov) for further information
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                                                                                                                                                                                                                   primer: -40RP from Gibco
                                                                                                                                                                                                  quality sequence stop:
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE:482524"
/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: p777T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st str was primed with a Not I - oligo(dT) primer [5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gatctacctcggaaccccgcctcaagagttcaccgttctcttttgatactggttcctctga 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGGTCACCAGGATCCCCCTGCACAAAGGGAAGTCTCTGAGGAACACCCTGAAGGAGCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGTAGAATGGAGGGCTTCCTGGCCTACGACACTGTCACAGTCTCTGATATTGTAGTGTN 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aggtagcatgcaaggaatcttaggctatgataccgtcactgtctccaacattgtggacat 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATCTACATTGGGACACCACCGCAGGAGTTCACCGTGGTGTTTGACACAGGCTCCTCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgagatcacccgcattcctctacaaaaggtaagtctctccgtaaggcgctgaaggaaca 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tccgagaaagtcgtccaccttccagaacttaggcaaacccttgtctatacactacggtac 437
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                                                                                                                                                                                         HTC; CAP trapper.

Mus musculus (strain:C57BL/6J) adult male stomach cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                                                                       AKO08959 1385 bp mRNA linear HTC 19-JAN-2002 Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210416016:homolog to GASTRICSIN PRECURSOR (EC 3.4.23.3) (PEPSINOGEN C), full insert sequence.
    Carninci, P., Sh
Itoh, M., Konno,
                                                          99279253
                                                                                Meth.
                                                                                                         Carninci
                                                                                                                                                                      Mus
                                                                                                                                                                                                                           AK008959.1 GI:12843460
HTC; CAP trapper.
                                                                                                                                                                                                                                                            AK008959
                                                                                           High-efficiency
                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                    clone: 2210416016.
                                                10349636
                                  (sites)
                                                                                                                          (sites)
                                                                                                                                                                    musculus
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                                                                           Enzymol.
                                                                                                         ,P. and Hayashizaki,Y.
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10,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,
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                                                                           full-length cDNA cloning
103, 19-44 (1999)
                                                                                                                                     Chordata;
Rodentia;
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Pred. No. 4.2e-58;
D; Mismatches 132
                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                516
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                         Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409, 685-690 (2001)
5 (bases 1 to 1385)
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e RIKEN Genome
/tissue_type="stomach"
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                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="MGD:MGI:1895643"
/db_xref="taxon:10090"
                                                                                                                 /clone="2210416016"
                                                                                      /sex="male"
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                                    TACCTTGGCAGCCAGCAGGGGTCTAACGGCGGGCAGATTGTGTTCGGTGGCGTGGACGAG
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Pred. No. 4.2e-56;
0; Mismatches 483
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                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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MR1-SN0064-150500-004-a03
                                                                                                                    This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=WR1-SN0064-150500-004-a03&t3=2000-05-15&t4=1)
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                                                                                                                                                                                                                                                                                                                                                                           sequence tags
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Fax: +55-11-2707001
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quality sequence stop: (
Location/Qualifiers
/organism="Homo sapiens"
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Eutheria;
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                                                                                                                                                                                                                                        AK008886 1388 bp mRNA linear HTC 19-JAN-2002 Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210410L06:homolog to GASTRICSIN PRECURSOR (EC 3.4.23.3) (PEPSINOGEN C), full insert sequence.
                                                                                                       Mus musculus (strain:C57BL/6J) adult male stomach cDNA to clone_lib:RIKEN full-length enriched mouse cDNA library
                                                            Mus musculus
                                                                                    clone: 2210410L06.
                                                                                                                                                              AK008886.1 GI:12843349
HTC; CAP trapper.
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/dev_stage="Adult"
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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     source
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CE 5 (bases 1 to 1388)

CE 5 (bases 1 to 1388)

R. Arakawa, T., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Kato, H., Kawai, J., Kojima, Y., Toh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Toh, M., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Salto, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schrimi, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Ninogaki, Y., Toya, T., Yamamura, T., Yamanaka, I., Payashizaki, Y., Shinaka, K., Yoshino, M., Muramatsu, M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission

Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohan Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Tel:81-45-503-9222,
                                                                                                                                                                         URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/)
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                                                                            Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999)
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                       ggttcctctgacttctgggttccctctatctactgcaagagcaatgcctgcaagaaccac
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                                                                                 ATCCAGGTCCCTAACCAGGAGTTCGGCCTGAGTGAGAATGAGCCTGGCACCAATTTTGTC
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SQGGSNGGQIVFGGVDENLYTGELTMIPTVTGLYWQITDLGNQASGGCSSGGC
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GIVDTGTSLLYMPAQYINELLQTIGAQEGEYGQYFVSCDSVSSLPTLTFVLNGVQFPL
SPSSYIIQEEGSCMVGLESLSLNAESGQPLWILGDVFLRSYYASSTWAITGWALPLLS
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/db_xref="MGD:MGI:1895666"
/db_xref="taxon:10090"
/clone="2210410L06"
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/clone_lib="RIKEN full-length
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Du
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,F
                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                    Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. La
                                                                                                                                                                                                                                                                                                         Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                 This read is a RESEQUENCE of This read has been verified
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ALIGNMENTS

AAU00536 ID AAU0

AAU00536 standard; Protein;

390

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AAU00536;

14-MAY-2001 (first entry)

RESULT

1

Key Peptide Chymosin; transcription regulator; terminator sequence; soybean; corn; rape seed; sunflower; cotton; tobacco; alfalfa; wheat; barley; oats; sorghum; Arabidopsis thaliana; potato; flax; linseed; rice; safflower; oil palm; ground nut; Brazil nut; coconut; castor; coriander; squash; oil palm; ground nut; Brazil nut; coconut; WO200114571-A1 Peptide Bos sp. Bovine chymosin polypeptide sequence. 23-AUG-2000; 2000WO-CA00975 Protein jojoba. Location/Qualifiers /note= "Pro sequence" 68..390 /note= "Signal peptide" 27..67 "Mature chymosin"

23-AUG-1999;

99US-0378696

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                                 Kluyveromyces;
                                                    BamHI/Sall insert of Kluyveromyces plasmid pAB309
                                                                           15-JUN-1990
                                                                                                                    AAP94376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing chymosin in seeds of plants such as rice, flax, rape seed, by transforming plant cell with a nucleic acid encoding chymosin operably linked to transcription regulator and terminator sequences -
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                                                                                                                                                                        SYYTGSLHWYPYTVQQYWQFTVDSVTISGVVVACEGGCQAILDTGTSKLYGPSSDILNIQ
                                                                                                                                                                                                                                                                                                                                          nhqrfdprksstfqnlgkplsihygtgsmqgilgydtvtvsnivdiqqtvglstqepgdv
                                                                                                                                                                                                                                                                                                                                                                                                                                          MNFLKSFPFYAFLCFGQYFVAVTHAAEITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGI
                                                                                                                                                                                                                 qaigatqnqygefdidcdnlsymptvvfeingkmypltpsaytsqdqgfctsgfqsenhs
                                                                                                                                                                                                                           QAIGATQNQYGEFDIDCDNLSYMPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQSENHS
                                                                                                                                                                                                                                                                                                   FTYAEFDGILGMAYPSLASEYSIPVFDNMMNRHLVAQDLFSVYMDRNGQESMLTLGAIDP
                                                                                                                                                                                                                                                                                                                                                       NHQRFDPRKSSTFQNLGKPLSIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDV
                                                                                                                                                                                                                                                           syytgslhwvpvtvqqywqftvdsvtisgvvvaceggcqaildtgtsklvgpssdilniq
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                                                                                                                                                                                                                                                                                                                                                                                                                                mnflksfpfyaflcfgqyfvavthaaeitriplykgkslrkalkehglledflqkqqygi
                                                                                                                                                                                                                                                                                                                                                                                      sskysgfgevasvpltnyldsqyfgkiylgtppqeftvlfdtgssdfwvpsiycksnack
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                                                                                                                    standard;
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                                                                          (first entry)
            lactis
                                 PDM100PC;
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                                                                                                                    protein;
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                                 chymosin;
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Pred. No. 6.6e-187;
Mismatches 0;
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                                 tissue
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                                plasminogen
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Oleosin-spacer-Met-prochymosin
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                      29-NOV-1999
                                                              AAY33830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP301670-A.
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                                                                                                                                                            392
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DB; AAN91188.
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                                                                                                                                      VGLAKAI 390
                                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity
366; Conserv
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                                                              standard;
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                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
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                                                             Protein;
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amino acid sequence

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Kluyveromyces host cells for producing polypeptide(s) - used for highly efficient prodn. of eg chymosin tissue plasminogen activator or human serum albumin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; ; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kluyveromyces expression systems processing of a wide variety of p
                                                                                                                                        HAAEITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASVPLTNYLDSQY
                                                                                                                                                                                                     svtisgvvvaceggcqaildtgtsklvgpssdilniqqaigatqnqygefdidcdnlsym
                                                                                                                                                                                                                      SVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYM
                                                                                                                                                                                                                                                                                                                                                                                               FGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                            \verb|hmaeitriply| kgkslrkalke| hglledflqkqqygisskysgfgevasvpltnyldsqy|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eromyces expression systems provide highly ssing of a wide variety of proteins. identical to those published in EP301669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.78;
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 incorporated into plasmids pAB309 with 18 resistance marker fused to a ADH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rietveld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 10;
2.2e-174;
hes 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     efficient secretion
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                                                                                  Query Match
Best Local S
Matches 368
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16-NOV-1993;
30-DEC-1994;
                                                                                                                                                                  glycanases, hormones, proteases, protease inhibitors, seed stora proteins, thrombin inhibitors, hirudin, interleukins, chymosin, xylanase, carp growth hormone, zein or a collagenase. The enzyme may be cleaved from the oil body protein or used in association with the oil body fraction.

Allows production of commercially important proteins on a superito protein on be easily separated from host cell components due to the use of the oil body as a carrier protein.
                                                                                                                                                                                                                                                                                                                       This is the amino acid sequence of a HindIII fragment containing the oleosin-spacer-Met-prochymosin sequence. This HindIII fragment was joined to a nopaline synthase terminator and cloned into binary vector pcGN1559. The resulting plasmid was called psBSOTPTNT and introduced into A.tumefaciens. The resulting bacterial strain was used to transformance.
                                                                                                                                                                                                                                                                          oil-body targeting sequence, a transcription regulation sequence and DNA of the protein of interest can be used to produce antibodies,
                                                                                                                                                                                                                                                                                               B.napus plants.
The DNA which encodes a chimeric fusion protein that consists of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oil-body; lipid bo
fusion protein; he
plasmid; oil-body
                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       Expression of a heterologous polypeptide on an oil body protein useful for the production of e.g. enzymes, antibodies, hormones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
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                                                                                                                                                                                                                                                                                                                                                                                                 Example 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moloney
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-1997;
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                                    169
            74
                                                          16
                                PLTNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTF
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Similarity
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91US-0659835.
93US-0142418.
94US-0366783.
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182..483
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176..181
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119..175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                              48pp;
                                                                                            93.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Thrombin cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Met-Prochymosin
                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                 Score 1928; D
Pred. No. 8.3e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  targeting
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                                                                                             DB 20;
3.3e-174;
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                                                                                                      Length
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RESULT
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              Also claimed is E.coli JM83/pLC7 (ATCC 39325) which is transformed with pLC7 contg. the prorennin derived sequence fused in phase with B-galactosidase. The pLC7 prorennin expression plasmid includes sequences which code for both the pseudorennin and mature rennin cleavage sites between AAs 28-29 and AAs 42-43, respectively.
Sequence
                                                               Claim
                                                                              Recombinant DNA coding for 
expressed in transformed
                                                                                                       N-PSDB;
                                                                                                                                                                             30-MAR-1984;
                                                                                                                                                                                             07-NOV-1984.
                                                                                                                                                                                                                                                   Key
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                                                                                                                                                                                                                                                                                                                  04-FEB-1992
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                                                                                                                                            (CODO-)
                                                                                                                                                             31-MAR-1983;
                                                                                                                                                                                                             EP123928-A.
                                                                                                                                                                                                                            Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VQQYWQFTVDSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pltnyldsqyfgkiylgtppqeftvlfdtgssdfwvpsiycksnacknhqrfdprksstf
                                                                                                                                                                                                                                                                                                                                                                                         ysvfdrannlvglakai
                                                               10;
                                                                                                                                            CODON GENETIC
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                                                                                                       AAN40295
                                                              Fig
381
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                                                                                                                              McCaman
                                                                                                                                                                                                                                                                                                                  (first
                                                              2;
                                                                                                                                                                                                                                                                                                  polypeptide displaying
AA;
                                                                                                                                                             83US-0480860
                                                                                                                                                                             84EP-0103551
                                                                                                                                                                                                                                                                                    recombinant
                                                                                                                                                                                                                            /label=
17..381
                                                                                                                                                                                                                                                   Location/Qualifiers
                                                              39pp;
                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                  entry
                                                                                                                              Ţ,
                                                                                                                                              ENG
                                                                              for milk clotting ed bacteria
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                                                              English.
                                                                                                                                                                                                                                   signal
                                                                                                                             Rice
                                                                                                                                                                                                                                                                                   protein;
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                                                                                                                                                                                                                                                                                                  milk clotting activity
                                                                                      polypeptide -
                                                                                       which
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Query Match Best Local Similarity

93.1%; 98.4%;

Score Pred.

1922; DB 5; No. 1.8e-173;

Length 381;

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RESULT
AAP40078
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The inventors claim the prochymosin gene comprising a nucleotide sequence from (a) the 1st codon (GCT) to the 365th codon (ATC), or (b) the 5th codon (CGG) to the 365th codon (ATC); and recombinant plasmids harboured by Escherichia coli strains deposited as FERM BP-262, -263 and -264. Any portion of the nucleotide sequence as described in AAN40055 can be used. Also claimed is a vector derived from plasmid pBR322. Typically plasmid pCR501 is obtd. from pOCT 2.
                                                                                              Expression useful for
                                                                                                                           N-PSDB;
                                                                                                                                    WPI; 1984-258001/42
                                                                                                                                                       Hidaka
                                                                                                                                                              Beppu T,
                                                                                                                                                                                                                       07-MAR-1984;
                                                                                                                                                                                                                                                                                                Prochymosin
                                                                                                                                                                                                                                                                                                                   Sequence encoded
                                                                                                                                                                                                                                                                                                                                     02-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                           AAP40078
                                                                                                                                                                                (BEPP/) BEPPU
                                                                                                                                                                                                     09-MAR-1983;
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                                                                                                                                                                                                                                                           EP121775-A.
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                                                                                           plasmid comprising prochymosin gene transforming Escherichia coli for pr
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                  DNA segment contg. GAL1 direction of expression
                                                                              N-PSDB;
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| nnlvglakti 375
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DB; AAN40180.
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                                                                                                                                                                                                   COLLABORATIVE RES INC
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98.4%;
                                                                                                                                       Fink
CG;
                  promoter linked to gene -
of the gene in yeast cell
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Pred. No. 2.
                                                                                                                                                            GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                          promoter;
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Mismatches
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?.2e-173;
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                                                                                                                                                                                              AAP94144 standard;
                                                                                                               proteinase;
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                         (NEZU-) NEDERL INS ZUIVELON
                                                                                              NL8701378-A
                                                                                                                        Lactic acid bacteria;
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       AFM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            are new.
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                                                                                                               pSK112;
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       De
                                                                                                                                                          (first entry)
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                                                            87NL-0001378
       Vos
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                                                                                                                                                                                             protein;
                                                                                                               a; cheese;
chymosin;
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                                                                                                                                                                                               365
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Pred. No. 3.5e-173;
2; Mismatches 4; Indels
                                                                                                              Streptococcus cremoris prochymosin.
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Matches 364
                                              Key
Region
                                                                                             Milk-clotting; cheese making;
                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The DNA encoding prochymosin can be cloned into a plasmid (esp. from S. cremoris SK112) and used to produce large amts of the protein by recombinant DNA techniques. This could overcome shortages of prochymosin due to a shortage of calf stomachs and increasing cheese prodn. Prochymosin is also used in prodn. of yoghurt, butter and buttermilk. See also AAP94145 and AAP94146.
                            Region
                                                                                                                                     03-AUG-1992
                                                                                                                                                        AAP30446;
                                                                                                                                                                            AAP30446 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; ; 43pp; Dutch.
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N-PSDB; AAN91157.
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                                                                                                                                                                                                                                                             VVFEINGKMYPLTPSAYTSQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDRANNLVG
                                                                                                                                                                                                                                                                                                                                          LAKAI 390
                                                                                                                                                                                                                                                                                                                TISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYMPT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                KIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYG
                                                                                                                                                                                                                                                                                                      tisgvvvacergcqaildtgtsklvgpssdilniqqaigatqnqygefdidcdnlsympt
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364; Conserv
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/label=
59..381
/label=
                             1..16
/label=
17..58
                                                        Location/Qualifiers
                                                                                                                 γď
                                                                                                                 preprochymosin cDNA
                                                                                                                                     entry)
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                  prochymosin
                                     preprochymosin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specific for lactic microorganism used i cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1918; DB 10;
Pred. No. 4.1e-173;
0; Mismatches 1;
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Matches 364; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                            The inventors claim a method for the prodn. of calf stomach chymosin for cheese making. Genes and polypeptides for preprochymosin, prochymosin and chymosin are claimed, as are vector systems and a prochymosin primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prodn. or calf stomach chymosin for cheese cultivation of micro-organisms transformed
                Pre-prorennin-A
                                                                AAP20038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUN-1982;
                                16-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                      YSIPVFDNMMNRHLVAQDLFSVYMDRNGQESMLTLGAIDPSYYTGSLHWVPVTVQQYWQF
                                                                                                                                                                                                                                               SIHYGTGSMQGILGYDTYTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASE
                                                                                                                                                                                                                                                                                SQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPL 140
                                                                                                        nnlvglakai 381
                                                                                                                 NNLVGLAKAI
                                                                                                                                                                       TVDSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNL
                                                                                                                                                                                                       ysipvfdnmmnrhlvaqdlfsvymdrigqesmltlgainpsyytgslhwvpvtvqqywqf
                                                                                                                                                                                                                                        sihygtgsmqgilgydtvtvsnivdiqqtvglstqepgdvftyaefdgilgmaypslase
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                                                                 standard;
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                                                                                                                                                                                                                                                                                                                                                                               381 AA;
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                                (first
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rennin;
                protein sequence.
                                                                 Protein;
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prorennin;
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                                                                                                                                                                                                                                                                                                                                       Score 1918; DB 4;
Pred. No. 4.3e-173;
3; Mismatches 3;
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enzyme;
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EC-3.4.23.4;
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RESULT 1
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        AAR05080;
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SQXCCCCCXXXT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       appropriate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transformed cells producing rennin and appropriate recombinant DNA material
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16-JAN-1981;
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                                                                                               symptvv feingkmypltps ayts qdqgfctsgfqsenhsqkwilgdvfireyysvfds and the symptotic of the s
                                                                                                                             SYMPTYVFEINGKMYPLTPSAYTSQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDRA 380
nnlvglakai
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81US-0225717.
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98.1%;
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Pred. No. 1e-172;
2; Mismatches 5; Indels
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protein;

05-OCT-1990

(first entry)

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RESULT 1
AAP30603
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AC AAP3
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Best Local S
Matches 362
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plasmid
Sequence encoded by prorennin cDNA in pCR 10001
                  14-JUN-1992
                                AAP30603;
                                                AAP30603 standard;
                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
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N-PSDB; AAQ04683.
                                                                                                                                                                                                                                                                                                                                                                                                        Complex plasmid and microbe -
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les 362; Conserv
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                                                                                                      LAKAI 390
                                                                                                                                                          TISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYMPT
                                                                                                                                                                                                               tgsmqgilgydtvtvsnivdiqqtvglstqepgdvftyaefdgilgmaypslaseysipv
                                                                                                                                                                                                                                                       KIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYG 145
                                                                                                                                                                                                                               TGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSIPV 205
                                                                                                                                                                                                                                              kiylgtppqeftvlfdtgssdfwvpsiycksnacknhqrfdprksstfqnlgkplsihyg
                                                                                                                                                                                                                                                                                                                                                                   product may be pBR322.
                                                                                                                                                                                                                                                                                                                                                     365
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                 (first entry)
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                                               Protein;
                                                                                                                                                                                                                                                                                                                    92.5%;
                                                                                                                                                                                                                                                                                                                                                                                          Japanese.
                                                                                                                                                                                                                                                                                                                                                                           expressed
                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                   Score 1910; DB 11;
Pred. No. 2.3e-172;
                                                                                                                                                                                                                                                                                                                                                                                                        contains calf pro-rennin
                                                                                                                                                                                                                                                                                                             Mismatches
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RESULT 1
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Best Local S
Matches 361
                                                                                                                                                                                                                                                                                                                                                                                               The inventors claim recombinant plasmids contg. the cDNA of calf prorennin. Specified plasmids are pCR 10001 and pCR2001 (contg. the whole sequence plus the lac promoter region). Also new are microorganisms transformed with the plasmids, esp. E. coli CR1 (ATCC 391710) contg. plasmid pCR2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Page 20-23; 32pp;
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                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BEPP/) BEPPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-AUG-1982;
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                                                                                                                                                                 266
                                                                                                                                                                                   181
                                                                                                                                                                                                                      121
                                                                        361
                                                                                                                                               241
                                                                                                                                                                                                     206
                                                                                                                                                                                                                                         146
                                                                                                                                                                                                                                                                                                                                  Local Sim hes 361;
                                                                                                                                                                                                                                                          61 kiylgtppqeftvlfdtgssdfwvpsiycksnacknhqrfdprksstfqnlgkplsihyg
                                                                                                                                                                                                                                                                                                                 26
                                             12
                                                                                                                                                                                                                                                                                            1983-22976K/10.
DB; AAN30063.
                                                                                         LAKAI 390
                                                                                                        TISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYMPT 325
                                                                                                                                                                                AEITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASVPLTNYLDSQYFG 85
                                                                                                                                                                                                                                                                   KIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYG 145
                                                                                                                                             tisgvvvaceggcqaildtgtsklvgpssdilniqeaigatqnqydefdidcdnlsympt 300
                                                                                                                                                                                                                                                                                                                                 Similarity 98.9
61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Uozumi T,
                                                                        365
                                                                                                                                                                                                                                                                                                                                                                                365
                                                                                                                                                                                                                                                                                                                                                                                A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81JP-0131631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82EP-0107601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pro:rennin DNA
                                                                                                                                                                                                                                                                                                                                          92.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
                                                                                                                                                                                                                                                                                                                                 Score 1907; DB 4;
Pred. No. 4.5e-172;
1; Mismatches 3;

    and transformed

                                                                                                                                                                                                                                                                                                                                                 Length 365;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                 Gaps
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0

AAP30013;

AAP30013 standard;

peptide;

379

B

381

AA

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RESULT 1
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                                       В
                                                QΨ
                                                          Вb
                                                                               밁
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                                                                                                                                                              Query Match
Best Local S
Matches 362
                                                                                                                                                                                             from calves, and plasmids contg. the genes which are capable of replicating in a prokaryotic organism. The prokaryotic organism is pref. an Escherichia species, esp. E. coli p Gx 1225 (NRRL B-15061). The microorganisms transformed by the plasmid are also claimed.
                                                                                                                                                                                                                                                                                                             03-NOV-1983
                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                    13-APR-1983;
01-JUL-1982;
                                                                                                                                                                                                                                                                                                   30-JUN-1983;
                                                                                                                                                                                                                                                                         (GENE-) GENEX
                    370
                             381
                                                                                190
                                                                                                   130
                                                 321
                                                                      261
                                                                                         201
                                                                                                             141
                                                                                                                                                              hes 362;
                                                            250
                                                                                                                                81
                                                                                                                                          10
     13
                                                                                                                                                                                                                                       lated chymosin or rennin and prochymosin gench replicate in prokaryotic organisms, esp. organisms used for chymosin biosynthesis
                                                                                                                                                                                                                                                                                                                                taurus
                                                           nnlvglakai
                             NNLVGLAKAI 390
                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                              enzyme;
                                                                                                                                                                                                                              Page 33-36; 43pp; French.
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                          CORP
                                                                                                                                                                                                                                                                                    83US-0484539
82US-0394433
                                                                                                                                                                                                                                                                                                   83BE-0017731
                                                                                                                                                                                                                                                                                                                                              zymogen;
                                                                                                                                                                   92.2%;
                                                                                                                                                                                                                                                                                                                                               rennin; chymosin;
                                                                                                                                                              Score 1903; Depred. No. 1.1e
3; Mismatches
                                                                                                                                                              DB 4;
1.1e-171;
hes 5;
                                                                                                                                                                                                                                                                                                                                               cheese
                                                                                                                                                                                                                                             Escherichia
                                                                                                                                                                       Length 379;
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                                                                                                   189
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                                  멂
                                           Qy
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                                                                           Ъ
                                                                                    δÃ
                                                                                                                                           В
                                                                                               Вb
                                                                                                                  Query Match
Best Local S
Matches 361
                                                                                                                                                                                                                                                                                                                                 Sequence
allelic f
                                                                                                                                                                                                                                                                      20-APR-1983
                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                           Sequence
                                                                                                                                                                                                                                        (UNIL )
                                                                                                                                                                                                                                                                                                             Bos taurus
                                                       132
                                   192
                                                                 141
                                             201
                                                                                     81
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DNA molecules comprising genes for preprochymosin - utransform microorganisms to give strain producing the prepro-enzyme and its allelic and maturation forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                      clotting component of renne AAN30049 corresp. to mRNA i preruminant calf (abomasum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preprochymosin is an intermediate (via prochymosin and pseudochymosin) for the enzyme chymosin, which is the essential pseudochymosin of rennet and is used in cheese manufacture. AAN30049 corresp. to mRNA isolated from the fourth stomach of a
               321
                                                                                                                                                                                                                                                                                    SIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEEDGILGMAYPSLASE
                                                                                                                                                                                                                            SYMPTYVFEINGKMYPLTPSAYTSQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDRA
                                                                                                                                                                 sihygtgsmqgilgydtvtvsnivdiqqtvglstqepgdvftyaefdgilgmaypslasq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNILEVER
                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                   Conservative
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1..16
/label= signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by cDNA sequence corresponding ) of bovine preprochymosin.
                                                                                                                                                                                                                                                                                                                                                                 92.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ledeboer
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                                                                                                                                                                                                                                                                                                                                                                 Score 1903;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΑM,
                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                 ; DB 4;
1.1e-171;
hes 6;
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                                                                                                                                                                                                                                                                                                                                                                              Length 381;
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312

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RESULT 14
AAR20730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
The prorennin (prochymosin) sequence was deduced from the DNA sequence obtd. by screening a cDNA library with rennin specific probes derived from the published amino acid sequence of rennin (Foltmann et al., J. Biol. Chem. 254, 8447-8456 (1979)) (see 233291,2). The deduced protein sequence was the same as the published sequence after cleavage of the signal peptide, except for an amino acid change at residue 218, which may be an artefact of protein sequencing in the original sequence. The cleavage product of prorennin, rennin is synthesised in two active forms rennin A, and rennin B. The cleaved
                                                                                                                                                                                                                                                                          28-OCT-1988;
11-MAY-1984;
12-DEC-1986;
31-MAR-1983;
                                                                                                                        Disclosure;
                                                                                                                                                      Isolating heterologous polypeptide from bacterial inclusion bodies - by lysing cells, extn. with nonionic detergent and
                                                                                                                                                                                                                                                                                                                                 28-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                      21-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cleavage-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prochymosin (prorennin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAY-1992
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                                                                                                                                                                                                                                            (BERL-)
                                                                                                                                                                                                                                                                 28-APR-1986;
                                                                                                                                            insoluble polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NNLVGLAKAI 390
|||||||||||
2 nnlvglakai 381
                                                                                                                                                                                      1992-049149/06.
DB; AAQ20949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           symptvvfeingkmypltpsaytsqdqgfctsafqsenhsqkwilgdvfireyysvfdra 371
                                                                                                                                                                                                                      MŢ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             zymogen; au
g activity;
                                                                                                                                                                                                                                            BERLEX LABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                      Fig 6; 21pp; English.
                                                                                                                                                                                                                     King
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                               88US-0263927.
84US-0609495.
86US-0940199.
83US-0480860.
86US-0856700.
                                                                                                                                                                                                                                                                                                                                88US-0263927
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
306
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59..60
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1..381
                                                                                                                                                                                                                                                                                                                                                                                                           218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= signal_peptide
43..44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label- preprorennin
/note- "also known as preprochymosin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autocatalytic activation; pseudorennin; milk;
y; renin A, renein B.
                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                      JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein; 381
                                                                                                                                                                                                                                                                                                                                                                                              "Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "autocatalytic cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                   "amino acid determining of rennin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "autocatalytic cleavage
                                                                                                                                                                                                                                                                                                                                                                                              in published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                sequence'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  pH 4.7"
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Best Local S
Matches 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stomach to generate mature rennin by two autocatalytic cleavage events. Rennin is an active component of rennet which is used to clot milk in the process of making cheese. See also AAR22417.
            plasminogen
                    Kluyveromyces host cells for producing polypeptide(s) - used for highly efficient producing the composition of eachymosin tissue
                                                                van den
                                                                                                                             01-JAN-1989
                                                                                                                                                                                                        AAP94370
                                                                                                                                                                                                                       AAP94370 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                (KONN)
                                                                                               28-JUL-1987;
                                                                                                              28-JUL-1988;
                                                                                                                                                          Kluyveromyces;
                                                                                                                                                                         Sequence encoded by
                                                                                                                                                                                         15-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                    132
                                                                                                                                                                                                                                                             371
                                                                                                                                                                                                                                                                           380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                           1989-033565/05.
DB; AAN91185.
                                                                                                                                                                                                                                                                                                                                                    annlvglakai
                                                                                                                                                                                                                                                                     ANNLVGLAKAI
                                                                                                                                                                                                                                                                                                  LSYMPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDR
                                                                                                                                                                                                                                                                                                                      SQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPL 140
                                                                                                                                                                                                                                                                                          lsymptvvfeingkmypltpsvytsqdqgfctsgfqsenhsqkwilgdvfireyysvfdr
                                                                Berg
                                                                                GIST-BROCADES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                JA,
                                                                                                                                                                                         (first
                                                                                                                                                          pDM100PC; chymosin; tissue plasminogen activator
                                                                                               87US-0078539
                                                                                                              88EP-0201632
                                                                                                                                                                                                                                                                           390
                                                                                                                                                                                                                                                             381
                                                                van
                                                                                                                                                                                                                      protein;
                                                                                                                                                                         BamHI insert from pDM100PC
                                                                                                                                                                                         entry)
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                                                                                Ā
                                                                Ooyen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                AJJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                 Rietveld
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             381;
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                                                                                                                                                                                                                                                                                                                                                                     259
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Disclosure; ; 56pp; English

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                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 355
                                                                                                                                                                                                                                                                                                                                                                    The pDM100PC sequence product comprises a fusion peptide of the alpha-factor of 5.cerevisiae and prochymosin and transcriptional and regulatory control regions. The Kluyveromyces expression systems provide highly efficient secretion and processing of a wide variety of proteins. Sequences identical to those published in EP301669.
                                                                                                                                                                                                                                                                                                                                                    Sequence
                      380
                                           380
                                                                                  320
                                                                                                       260
                                                                                                                            260
                                                                                                                                                 200
                                                                                                                                                                     200
                                                              320
                                                                                                                                                                                         140
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                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                       80
                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                Match 90.8%;
Local Similarity 95.7%;
ses 355; Conservative
|||||||||||
|pnnlvglakai 450
                                        FTVDSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDN 319
                                                                                                                          LSIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLAS
                                                                                                                                                                                                            ANNLYGLAKAI 390
                                                              LSYMPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDR 379
                                                                                  ftvdsvtisgvvvpceggcqaildtgtsklvgpssdilnigqpigatqnqygdfdidcdn
                                                                                                                                                                                                                                                                                                                                                     450 AA;
                                                                                                                                                                                                                                                                                                Score 1874; DB 10;
Pred. No. 8.2e-169;
5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                    Length 450;
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                 0;
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Search completed: July 31, 2002, 09:20:52 Job time: 1554 sec

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                      Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
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PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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2064
                                                                                                     Listing first 45 summaries
                                                                                                                       Maximum Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                    July 31, 2002, 09:16:08; Search time 20.9 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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pir2:*
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                                                                                                                                                                                                                                                                                                                                                                                                                (without alignments)
1793.055 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

pir4:*

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	5	4	ω	N	_		Result
892	894	911.5	918	923	930	942.5	957.5	1016.5	1030	1034	1037	1045	1070	1074	1075.5	1078.5	1080.5	1082.5	1084.5	•	1092.5	1094.5	1099.5	1108.5	1601	1605	1829	1932	00016	200
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A; Molecule type: protein A; Residues: 17-173,'T',175-217,'D',219-251,'Y',253-381 <FO2> R; Chang, W.J.; Takahashi, K. J. Biochem. 76, 467-474, 1974

A; Title: The structure and function of acid proteases. III. Isolation and characteriz

A;Molecule type: protein
A;Residues: 59-217, D', 219-381 <FOL>
R;Foltmann, B.; Pedersen, V.B.; Jacobsen, H.; Kauffman, D.; Wybrandt, Proc. Natl. Acad. Sci. U.S.A. 74, 2321-2324, 1977
A;Title: The complete amino acid sequence of prochymosin.
A;Reference number: A44620; MUID:77234648
A;Accession: A44620

J. Biol. Chem. 254, 8447-8456, 1979
A; Title: The primary structure of calf chymosin.
A; Reference number: A92259; MUID:79239460

R;Foltmann, B.; Pedersen, V.B.; Kauffman, D.; Wybrandt, J. Biol. Chem. 254, 8447-8456, 1979

A; Note: authors translated

the codon TTG

for residue 43 as

Phe,

ACC

A;Contents: chymosin B; disulfide bonds A;Accession: A92259

ALIGNMENTS

N;Âlternate names: preprochymosin; preprorennin; rennin B N;Contains: chymosin; prochymosin C;Species: Bos primigenius taurus (cattle) C;Date: 24-Apr-1984 #sequence_revision 09-Sep-1994 #text_change 18-Jun-1999 C;Accession: A25631; A93419; A44608; A92259; A44620; A91935; A91495; D22434; A00985 R;Hidaka, M.; Sasaki, K.; Uozumi, T.; Beppu, T. Gene 43, 197-203, 1986 A;Title: Cloning and structural analysis of the calf prochymosin gene. A;Reference number: A25631; MUID:86301873 A;Accession: A25631 A;ACCESSION. A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-229 'N',231-381 <HAR> A;Residues: 1-229 'N',231-381 <HAR> A;Cross-references: GB:J00003; NID:g162859; PIDN:AAA30448.1; PID:g162860 A;Residues: 1-16,'T',18-381 <HID> R;Harris, T.J.R.; Lowe, P.A.; Lyons, A.; Thomas, P.G.; Eaton, M.A.W.; Millican, T.A.; Nucleic Acids Res. 10, 2177-2187, 1982 A;Title: Molecular cloning and nucleotide sequence of cDNA coding for calf preprochym A;Reference number: A33419; MUID:82221400 A; Molecule type: mRNA A; Residues: 7-14,'X',16-42,'L',44-87,'N',89-301,'D',303-324,'I',326-334,'G',336-342,'A; Cross-references: GB:J00004 chymosin (EC 3.4.23.4) precursor -A;Title: Nucleotide sequence of calf prorennin cDNA cloned in Escherichia coli. A;Reference number: A44608; MUID:82189915 A; Accession: A; Accession: A; Contents: prochymosin B A; Molecule type: DNA A44608 A93419 bovine

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A;Reference number: A91935; MUID:75060332
A;Accession: A91935
A;Accession: A91935
A;Accession: A91935
A;Rolecule type: protein
A;Residues: 92-96;274-278,280 <CHA>
A;Residues: 92-96;274-278,280 <CHA>
A;Residues: D; Asao, J; Schumm, J.W.; Vovis, G.F.; Alford, B.L.; Taunton-Rigby, A.
Residues: D; Mao, J; Schumm, J.W.; Vovis, G.F.; Alford, B.L.; Taunton-Rigby, A.
Residues: A91495; MUID:83054629
A;Title: Molecular cloning and characterization of double-stranded cDNA coding for ba
A;Reference number: A91495
A;Rolecule type: mRNA
A;Residues: 1-301, D',303-381 <MOID
A;Residues: 1-301, D',303-381 <MOID
A;Residues: 1-301, D',303-381 <MOID
A;Residues: 1-301, D',303-381 <MOID
A;Residues: 1-180, XX',21, YSC
A;Title: Isolation of human, swine, and rat prepepsinogens and calf preprochymosin, A;Reference number: A22444; MUID:86059312
A;Reference number: A22443; MUID:86059312
A;Recession: D22434
A;Recession: D22434
A;Recidues: 1-18, XX',21, XX',24, X',26, X',28, X',30 <ICH>
C;Comment: The sequence of variant B is shown.
C;Comment: The sequence of variant B is shown.
C;Comment: Enymosin is synthesized in the mucosa of the abomasum (fourth stomach) of C;Comment: Forms A and B are probably allelic variants. Chymosin B is the predominan C;Genetics:
A;Introns: 21/2; 71/3; 111/1; 150/3; 217/2; 255/2; 303/3; 336/3
C;Superfamily: pepsin
C;Reywords: aspartic proteinase; gastric Juice; hydrolase; protein digestion; stomac F;11-58/Domain: activation peptide #status experimental <APT>
F;92,274/Active site: Asp #status experimental Experimental
F;105-110,265-269,308-341/Disulfide bonds: #status experimental
chymosin (EC 3.4.23.4) B precursor - sheep
C; Species: Ovis orientalis aries, Ovis ammor
C; Date: 30-Sep-1991 #sequence_revision 30-
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A; Molecule type: mRNA
A; Residues: 1-381 <PUNN>
A; Residues: 1-381 <PUNN>
A; Residues: 1-381 <PUNN>
A; Cross-references: EMBL:x53037; NID:gl373; PIDN:CAA37209.1
A; Cross-references: EMBL:x53037; NID:gl373; PIDN:CAA37209.1
C; Superfamily: pepsin
C; Keywords: aspartic proteinase; gastric juice; hydrolase;
F; 1-16, Domain: signal sequence #status predicted <SIG>
F; 17-58/Domain: activation peptide #status predicted <APT>
F; 99.274/Arctive site: Asp #status predicted
F; 105-110, 265-269, 308-341/Disulfide bonds: #status predicte
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R;Pungercar, J.; Strukelj, B.; Gubensek, F.;
Nucleic Acids Res. 18, 4602, 1990
A;Title: Complete primary structure of lamb
A;Reference number: S10996; MUID:90356410
A;Accession: S10996
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A;Accession: JC7247
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                                                                             A; Molecule type: mRNA
A; Residues: 1-381 <KAG>
A; Cross-references: DDB
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C; Species: Callithrix jacchus (common marmoset)
C; Date: 09-Jun-2000 #sequence_revision 09-Jun-2
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Superfamily: pepsin; Keywords: gastric j
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Score

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DВ

2;

Length

381;

81.4%;

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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-380 <FOL> A;Cross-references: EMBL:U14406; NID:g540096; PIDN:AAB08492.1; C;Superfamily: peppin C;Keywords: aspartic proteinase; hydrolase
                                                                                                                                                                                                                                                                                                                   chymosin (EC 3.4.23.4) precursor - pig (fragment) C:Species: Sus scrofa domestica (domestic pig) C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 C:Accession: I47176 R:Foltmann, B: Jensen, A.L.: Loenblad, P.: Smidt, Comp. Biochem. Physiol. A 68, 9-13, 1981 A:Title: A Developmental Analysis of the Production A:Reference number: I47176 A:Accession: I47176
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                               LSIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLAS
                                                                                                                             DSQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTVDSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDN
                                                                                                                 DTQYFGKIYIGTPPQEFTVVFDTGSSELWVPSVYCKSDACQNHHRFNPSKSSTFQNLDKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVDSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASE
                                                                          LSIQYGTGSIQGFLGYDTVMVAGIVDAHQTVGLSTQEPSDIFTYSEFDGILGLGYPELAS
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                                                                                                                                                                                                   Score 1601; DB 2;
Pred. No. 8.8e-119;
5; Mismatches 39;
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D; Mismatches 39;
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pepsinogen A - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C:Date: 30-Jun-2001 #sequence_revision
C:Accession: JC7575
R; kuzawa, M.; Inokuchi, T.; Kobayashi,
J. Biochem. 129, 147-153, 2001
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R; Kageyama, T.

J. Biochem. 127, 761-770, 2000
A; Title: New world monkey pepsinogens A and C
A; Reference number: JC7245
A; Accession: JC7245
A; Molecule type: mRNA
A; Residues: 1-387 < KAG>
A; Cross-references: DDBJ: AB038384
A; Cross-references: DDBJ: AB038384
A; Experimental source: strain NW794
C; Comment: This protein, a zymogen of pepsins volution of mammalian orders and families.
C; Superfamily: pepsin
C; Keywords: gastric juice; zymogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pepsinogen A - common marmoset
C;Species: Callithrix jacchus (common m
C;Date: 09-Jun-2000 #sequence_revision
C;Accession: JC7245
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FDNMMNRHLVAQDLFSVYMDRNGQE-SMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTVDS
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FDNIWNQDLVSQDLFSVYLSSNDQSGSVVMFGGIDSSYYTGSLNWVPVSAEGYWQITVDS
                                                                                                                                                                                                                                                                                                                                   RIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGE----VASVPLTNYLDSQYFG
                                                                                                                                                                                        TGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSIPV
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30-Jun-2001 #text_change

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A;Gene: PgA
C;Superfamil
C;Keywords:
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A; Reference r
A; Contents: S
A; Accession:
                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-383 <HAY>
A; Cross-references: GB:D00215; NID:g2760810; PIDN:BAA00153.1;
C; Superfamily: pepsin
C; Keywords: aspartic protocol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-385 < IRV) >
A; Cross-references: DDBJ: ABO45376
C; Comment: This protein is a zymo
C; Genetics:
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                                                                                                                                                                                                                                                                                pepsin (EC 3.4.23.-) precursor, embryonic -
C;Species: Gallus gallus (chicken)
C;Date: 05-Jun-1992 #sequence_revision 05-Ju
C;Accession: A41443
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Best Loc
Matches
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                                                      Query Ma
Best Loc
Matches
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;Keywords: stomach;
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                          AFLCFGQYFVAVTHAAE-ITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKY-SGFG 68
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                                                         Mismatches
                                                                                                                                                                                                                                                                                                   05-Jun-1992 #text_change
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                                                                      1094.5;
No. 9.1e
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                                                3-79;
95;
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                                                                                                                                                                                                                                             for embryonic chicken per
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                                                                         TQNQYGEFDIDCDNLSYMPTVVFEINGKMYPLTPSAYTSQD-QGFCTSGFQSENHSQKWI
                                                                                                           FDGILGLGYPSLAADGITPVFDNMVNESLLEQNLFSVYLSREPMGSMVVFGGIDESYFTG
                                                                                                                                                                             FDGILGMAYPSLASEYSIPVFDNMMNRHLVAQDLFSVYMDRNGQESMLTLGAIDPSYYTG
                                                                                                                                                                                                                      \tt NPSQSSTYKSTGQNLSIHYGTGDMEGTVGCDTVTVASLMDTNQLFGLSTSEPGQFFVYVK
                                                                                                                                                                                                                                     DVLTVVTEPLLNTLDMEYYGTISIGTPPQDFTVVFDTGSSNLWVPSVSCTSPACQSHQMF
                                                                                                                                                                                                                                                                                           EVASV---PLTNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRF
               LGDVFIREYYSVFDRANNLVGLAKAI
                                                                                                                                      SLHWVPVTVQQYWQFTVDSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGA
LGDVFIRVYYSIFDRANNRVGLAKAI
                                                    NQNTYGEYSVNCSHILAMPDVVFVIGGIQYPVPALAYTEQNGQGTCMSSFQNSS-ADLWI
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in by 4 months of age.

C; Comment: Although two-step activation is observerd, activation is predomi C; Comment: Although two-step activation is observerd, activation is predomi C; Generically: pepsin proteinase; gastric juice; hydrolase; phosphoprotein; F; 11-5/Bomain: signal sequence #status predicted <SIG>F; 11-5/Bomain: signal sequence #status experimental <PPT>F; 16-388/Product: pepsinogen A 2/3 #status experimental <APT>F; 63-388/Product: pepsin A 2/3 #status experimental <PRZ>F; 63-388/Product: pepsin A 2/3 #status experimental <PRZ>F; 40-41/Cleavage site: Asp-Phe (pepsin) #status experimental F; 62-63/Cleavage site: Leu-Ile (pepsin) #status experimental F; 62-63/Cleavage site: Leu-Ile (pepsin) #status experimental F; 94-77/Active site: Asp #status predicted F; 107-112, 268-272, 311-344/Disulfide bonds: #status predicted F; 130/Binding site: phosphate (Ser) (covalent) #status predicted C;ACCESSION. T.; Tanabe, K.; Koiwai, U. R;Kageyama, T.; Tanabe, K.; Koiwai, U. Eur. J. Biochem. 202, 205-215, 1991
A;Title: Development-dependent expression
A;Title: Development-dependent expression
A;Title: Development-dependent expression pepsin A (EC 3.4.23.1) 2/3 precursor - Japanese N;Alternate names: pepsinogen A isozyme 2/3 C;Species: Macaca fuscata (Japanese macaque) C;Date: 22-Nov-1993 #sequence_revision 19-Oct-19 C;Accession: S19684; S16064 RESULT S19684 A;Cross-references: EMBL:x59755; NID:q38068; PIDN:CAA42427.1; PID:q38069 A;Note: parts of sequence, including amino ends of pepsinogen and activation intermed C;Comment: It could not be determined if this sequence represents isozyme 2 or 3, whi A; Molecule type: mRNA A; Residues: 1-388 < KAG> A; Accession: S19684 of -Oct-1995 #text_change isozymogens macaque of monkey 18-Jun-1999 is predominantly a pepsinogens protein and

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77

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Matches

Local Similarity

56.9%; 53;

score 1092.5;
Pred. No. 1.3e
53; Mismatches

..3e-7

Indels Length

9;

Gaps

ω

DB 1; 97;

Conservative

28

ITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASV----PLTNYLDSQY 83

ф QΥ В

137

YGTGSMTGILGYDTVQVGGISDTNQIFGLSETEPGSFLYYAPFDGILGLAYPSISSSGAT YGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSI 203 FGTIGIGTPAQDFTVIFDTGSSNLWVPSVYCSSLACTNHNRFNPQDSSTYQSTSGTVSIT FGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIH 143 IHKVPLVRKKSLRRNLSEHGLLKDFLKKHNFNPASKYFPQAEAPTLIDEQPLENYLDMEY 76

196

136

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A; Title: Cloning and sequencing of rhesus monkey pepsinogen A cDNA.
A; Reference number: JT0309; MUID:88313666
A; Accession: JT0309
A; Molecule type: mRNA
A; Residues: 1-388 <EVE>
A; Cross-references: GB:M20788; NID:g342274; PIDN:AAA36902.1; PID:g342275
C; Superfamily: pepsin
C; Keywords: aspartic proteinase; gastric juice; hydrolase; phosphoprotein
C; Keywords: aspartic proteinase; gastric juice; hydrolase; phosphoprotein
C; Keywords: aspartic proteinase; gastric juice (SIG)
F;16-3280/Product: pepsingen #status predicted <MATS
F:16-62/Domain: sciivation peptide #status predicted <APT>
F:63-388/Product: pepsin #status predicted <ENZ>
F:94,277/Active site: Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Macaca mulatta (rhesus macac
C;Date: 30-un-1999 #sequence_revision
C;Accession: JT0309
R;Evers, M.P.J.; Zelle, B.; Bebelman,
Gene 65, 179-185, 1988
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                                                                                                                                                                                                                                                                                                                                   YGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSI
                                                                                                                                                                                                                                                                                                                                                                                                            FGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIH 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPDIVETINGIQYPVPPSAYILQSQGSCISGFQGMDVPTESGELWILGDVFIRQYFTVFD
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  RANNQVGLA
                                      RANNLVGLA
                                                                            LPDIVFTINGVQYPLPPSAYILQSQGSCTSGFQGMDVPTESGELWILGDVFIRQYFTVFD
                                                                                                     MPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQS----ENHSQKWILGDVFIREYYSVFD
                                                                                                                                                   PVFDNIWDQGLVSQDLFSVYLSADDQSGSVVIFGGIDSSYYTGSLNWVPVSVEGYWQISV
                                                                                                                                                                                                                                                                       PVFDNMMNRHLVAQDLFSVYMDRNGQE-SMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTV
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                                                                                                                                                                                                                                                                                                           YGTGSMTGILGYDTVQVGGISDTNQIFGLSETEPGSFLYYAPFDGILGLAYPSISSSGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IYKVPLVRKKSLRRNLSEHGLLKDFLKKHNRNPASKYFPQTEAPTLIDEQPLENYLDVEY 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                        387
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57.2%;
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smatches 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eur. J. Biochem. 202, 205-215, 1991
A;Title: Development-dependent expression
A;Reference number: S19681; MUID:92037645
A;Mccession: S19681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Molecule type: protein
A; Residues: 41-261, /D', 263-388 <RA3>
A; Residues: 41-261, /D', 263-388 <RA3>
C; Comment: This is the major pepsin isozyme in juveniles and adversariation is a one-step process.
C; Superfamily: pepsin
C; Keywords: aspartic proteinase; gastric juice; hydrolase; phosp
F; 1-15/Domain: signal sequence #status predicted <SIG>
F; 1-15/Domain: activation peptide #status experimental <APT>
F; 63-388/Product: pepsin A 1 #status experimental <ENZ>
F; 94,277/Active site: Asp #status predicted
F; 107-112,268-272,311-344/Disulfide bonds: #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Monkey pepsinogens
A; Reference number: A91960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: parts of sequence, R;Kageyama, T.; Takahashi, J. Biochem. 88, 9-16, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pepsin A (EC 3.4.23.1) 1 precursor - Japanese macaque
N,Alternate names: pepsinogen A isozyme 1
C;Species: Macaca fuscatinogen A isozyme 1
C;Date: 13-Aug-1986 #sequence_revision 19-Oct-1995 #text_change 18-Jun-1999
C;Date: 13-Aug-1986 #sequence_revision 19-Oct-1995 #text_change 18-Jun-1999
C;Accession: S19681; A91960; A92579; A00981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;130/Binding site: phosphate (Ser) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A91960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X59752; NID:g38074; PIDN:CAA42424.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-388 < KAG>
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                                                                                                                                                                                                                                                                                                                                                RANNLVGLA
                                      LPDIVFTINGIQYPVPPSAYILQSQGSCTSGFQGMDVPTESGELWILGDVFIRQYFTVFD
                                                                                                                                   DSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSY
                                                                                                                                                                                                                                                                                               YGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSI 203
                                                                                                                                                                                                                                                                                                                                                                                                                            IYKVPLVRKKSLRRNLSEHGLLKDFLKKHNLNPASKYFPQAEAPTLIDEQPLENYLDVEY 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASV----PLTNYLDSQY 83
                                                                      MPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQS----ENHSQKWILGDVFIREYYSVFD 378
                                                                                                                                                                                            PVFDNIWDQGLVSQDLFSVYLSADDQSGSVVIFGGIDSSYYTGSLNWVPVSVEGYWQISV
                                                                                                                                                                                                                                                                         YGTGSMTGILGYDTVQVGGISDTNQIFGLSETEPGSFLYYAPFDGILGLAYPSISSSGAT 196
                                                                                                                 DSITMNGEAIACAEGCQAIVDTGTSLLTGPTSPIANIQSDIGASENSDGEMVVSCSAISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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MUID:86168132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 1084.5;
; Pred. No. 5.7e
52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7e-78;
ches 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hydrolase; phosphoprotein; protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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experimental

and adults

Indels Length

Gaps

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322 256

388; 9;

acid

and PID: 938075

activation

intermed

sequence of the activation

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monkey

pepsinogens

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N; Alternate r
C; Species: Hc
C; Date: 19-Fe
C; Accession:
                                                                                                                                                                                                                     A;Gene: GDB:PGA3
A;Gene: GDB:PGA3
A;Cross-references: GDB:119482; OMIM:169710
A;Map position: 11q13.1-11q13.5
A;Introns: 19/2; 73/3; 113/1; 152/3; 219/2; 258/2; 306/3; 339/3
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; gastric juice; hydrolase; phosphoprotein; [F;1-15/Domain: signal sequence #status experimental <SIG>F;16-388/Product: pepsinogen A 3 #status experimental <APT>F;16-388/Product: pepsin A 3, minor variant #status experimental <APT>F;60-388/Product: pepsin A 3, minor variant #status experimental <MIN>F;63-388/Product: pepsin A 3 #status experimental <APT>F;94,277/Active site: Asp #status predicted
F;130/Binding site: phosphate (Ser) (covalent) #status predicted
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A;Accession: A00980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 08-Dec-2000
C;Accession: A00980; PX0023; S02663; F22434; I54252; PX0024
C;Accession: A01980; PX0023; S02663; F22434; I54252; PX0024
R;Sogawa, K.; Fujii-Kuriyama, Y.; Mizukami, Y.; Ichihara, Y.; Takahashi, K.
J. Biol. Chem. 258, 5306-5311, 1983
A;Title: Primary structure of human pepsinogen gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-15, YXXY, 19-20, YX', 22, YXX', 25-26, YX', 28 <ICH>
R; Evers, M. P.J.; Zelle, B.; Peeper, D.S.; Mager, W.H.; Planta,
Hum. Genet. 77, 182-187, 1987
A; Title: Molecular cloning of a pair of human pepsinogen A gene
A; Reference number: 154252; MUID:88006181
A; Accession: 154252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Isolation of human, swine, and r. A;Reference number: A22434; MUID:86059312 A;Accession: F22434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 16-68 < FOL>
R; Ichihara, Y; Sogawa, K.; Ta
J. Biochem. 98, 483-492, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS Lett. 241, 69-72, 1988
A;Title: Activation of human pepsinogens.
A:Reference number: S02663; MUID:89065108
A;Accession: S02663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 16-100 < ATH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: A comparative study on the NH2-terminal A;Reference number: PX0023; MUID:90130402 A;Accession: PX0023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-388 <SOG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Athauda, S.B.P.; Tanji, M.;
J. Biochem. 106, 920-927, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pepsin A (EC
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A; Residues: 1-27, 'f', 29-73 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:J00279
                                                                                                                         Query Match
Best Local
                                                                                                      Matches
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19
                                                  30
                                                                                                                         Local Similarity
                                               RIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASV----PLTNYLDSQYFG 85
  KVPLIRKKSLRRTLSERGLLKDFLKKHNLNPARKYFPQWEAPTLVDEQPLENYLDMEYFG
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                                                                                                                         52.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takahashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kageyama, T.; Takahashi,
                                                                                                    52;
                                                                                                 Score 1082.5;
Pred. No. 8.2e
52; Mismatches
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                                                                                                 5; DB 1;
.2e-78;
.es 98;
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Matches

209;

Conservative

53;

Pred. No. 1.20 3; Mismatches

94;

Indels

13;

Gaps

4

Similarity

98 79

KIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYG 145

TIGIGIPAQDFTVLFDTGSSNLWVPSVYCSSLACTNHNRFNPEDSSTYQSTSETVSITYG

19

30 RIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASV----PLTNYLDSQYFG 85

KVPLIRKKSLRRTLSERGLLKDFLKKHNLNPARKYFPQWEAPTLVDEQPLENYLDMEYFG

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A;Cross-references: GDB:119483; OMIM:169720
A;Map position: 11q13-11q13
A;Introns: 19/1; 73/3; 113/1; 152/3; 219/2; 258/2; 306/3; 339/3
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; hydrolase; phosphoprotein; protein digestion; zymoge
F;1-15/Domain: signal sequence #status experimental <STO>
F;16-59/Domain: activation peptide #status experimental <APT>
F;63-388/Product: pepsin A 4 #status predicted <MAT>
F;94,277/Active site: Asp #status predicted
F;107-112,268-272,311-344/Disulfide bonds: #status predicted
F;107-spinding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: B30142; E22434
R;Evers, M.P.J.; Zelle, B.; Bebelman, J.P.; van Beusechem, V.; Kraakman, L.; Genomics 4, 232-239, 1989
A;Title: Nucleotide sequence comparison of five human pepsinogen A (PGA) gene A;Reference number: A91627; MUID:89233110
A;Accession: B30142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Nolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-27, 'F', 29-388 < EVE>
A; Note: the authors translated the codon TTC
A; Note: the authors K.: Takahashi, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pepsin A (EC 3.4.23.1) 4 precursor - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 20-Aug-1994 #text_change 29-Aug-1997
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B30142
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A; Residues: 1-15, 'XXX', 19-20, 'X', 22, 'XX', 25-26, 'X', 28
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J. Biochem. 98, 483-492, 1985
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Query Match
Best Local
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    Score 1080.5; DB Pred. No. 1.2e-77
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                         Length
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                           388;
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A; Molecule type: protein
A; Residues: 16-58 < RANN
R; Athauda, S.B.P.; Tanji, M.; Kageyama, T.; Takahashi, K.
J. Biochem. 106, 920-927, 1989
A; Title: A comparative study on the NH2-terminal amino acid sequence of the study o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Resident R;Bank, R.A.; Cru
R;Bank, R.A.; Cru
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N;Alternate names: pepsinogen 5
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 20-Aug-1994 #text_change 29-Aug-1997
C;Accession: A30142; S02564; S02542; PX0027; PX0025; PX0026; A22434
R;Evers, M.P.J.; Zale, B.; Bebelman, J.P.; van Beusechem, V.; Kraakman, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Foltmann, B. FEBS Lett. 241, 69-72, 1988
R;Tille: Activation of human pepsinogens.
A;Reference number: S02663; MUID:89065108
A;Accession: S02664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Bank, R.A.; Crusius, B.C.; FEBS Lett. 238, 105-108, 1988 A; Title: Identification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 16-68 <FOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-27,'F',29-388 <EVE>
A; Cross references: GB:M26025
A; Note: the authors translated the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Nucleotide sequence comparison of five human pepsinogen A (PGA) genes: A;Reference number: A91627; MUID:89233110
A;Accession: A30142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
A30142
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pepsin A (EC 3.4.23.1) 4 Previous Pepsin A (EC 3.4.23.1) 4 Previous Pepsin A isozyme 4 C;Species: Macaca fuscata (Japanese macaque) C;Date: 22-Nov-1993 #sequence_revision 19-Oct-1995 C;Accession: S19682; S16065 R.; Koiwai, O.
  F;1-15/Domain: signal sequence #status predicted <SIG>F;16-388/Product: pepsinogen A 4 #status experimental <PPT>F;16-62/Domain: activation peptide #status experimental <APT>F;63-388/Product: pepsin A 4 #status experimental <ENZ>F;38-39/Cleavage site: Leu-Lys (pepsin) #status experimental F;62-63/Cleavage site: Leu-Ile (pepsin) #status experimental
                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-388 < RAG:
A; Residues: 1-388 < RAG:
A; Cross-references: EMBL: X59753; NID: g38070; PIDN: CAA42425.1; PID: g38071
A; Note: parts of sequence, including amino ends of pepsinogen and activation C; Comment: This is a minor component of pepsin at all post-partum stages.
C; Comment: Although two-step activation is observerd, activation is predomina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 11q13-11q13
A;Introns: 19/1; 73/3; 113/1; 152/3; 219/2; 258/2; 306/3; 339/3
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; hydrolase; phosphoprotein; prote
F;1-15/Domain: signal sequence #status experimental <SIG>F;16-388/Product: pepsinogen A 5 #status experimental <ZYM>F;60-388/Product: pepsin A 5, minor variant #status experimental
F;63-388/Product: pepsin A 5 #status experimental <MAT>
F;94,277/Active site: Asp #status predicted
F;130/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
S19682
                                                                                                                     C; Superfamily: pepsin
C; Keywords: aspartic proteinase;
                                                                                                                                                                                                                                                                                                         Eur. J. Biochem. 202, 205-215, 1991
A; Title: Development-dependent expression
A; Reference number: S19681; MUID:92037645
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A; Cross-references: GDB:119484; OMIM:169730
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209; Conservative
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Leu-Lys (pepsin)
Leu-Ile (pepsin)
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Pred. No. 1.7e
51; Mismatches
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                                                                                                                        hydrolase; phosphoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                #text_change 18-Jun-1999
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                                                                                                                                                                                                                                                                                                                                 pepsinogens
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A;Molecule type: mRNA
A;Residues: 1-384 <IKU>
A;Cross-references: DDBJ:AB045380
A;Accession: pC7119
A;Accession: pC7119
A;Accession: pC7119
A;Residues: 16-35;57-76 <IK2>
C;Comment: This protein is a zymogen for gastric aspartic proteinase, with pepsin-like
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;94,277/Active site: Asp *status predicted F;107-112,268-272,311-344/Disulfide bonds: *status predicted F;130/Binding site: phosphate (Ser) (covalent) *status 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Amphibian pepsinogens: Purification and characterization of Xenopus pepsinogens A;Reference number: JC7573; MUID:21064922; PMID:11134969 A;Contents: Stomach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pepsinogen A - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
C;Accession: JC7574; PC7119
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Best Local Similarity
Matches 209; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                           ;Superfamily: pepsin
;Keywords: stomach; zymogen
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                                                                                                     VVKVPLRKGESFRNRPQRLGLLGDYLKKNPYNPASKYFPTLAQSSAETLQNYMDIEYYGT 75
                                                                                                                                                                ITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKY-SGFGEVASVPLTNYLDSQYFGK 86
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IYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYGT 146
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                                                                                                                                                                                                                                            52.0%; Score 1074; DB 2; Length 384; 54.6%; Pred. No. 3.8e-77; tive 64; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
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                                                VVFEINGKMYPLTPSAYTSQDQGFCTSGFQS----ENHSQKWILGDVFIREYYSVFDRAN 381
                                                                                                              TISGYVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYMPT 325
                                                                                                                                                                         DNMMNRHLVAQDLESVYMDRNGQE-SMLTLGAIDPSYYTGSLHWVPVTVQQYWQETVDSV
NLVGLA 387
                                                                                              SINGQVIACSQSCQAIVDTGTSLMTGPSTPIANIQNYIGASQDSNGQYVINCNNISNMPT
                                                                                                                                                                                                                     GSMSGFLGYDTLQVGNIQISNQMFGLSESEPGSFLXYSPFDGILGLAFPSIASSQATPVF 195
                                                                                                                                                                                                                                                                                  ISIGTPPQEFTVIFDTGSANLWVPSVYCSSQACSNHNRFNPQQSSTFQATNTPVSIQYGT 135
                                  IVFTINGVQYPLSPSAYVRQNQQGCSSGFQAMNLPTNSGDLWILGDVFIRQYFTVFDRAN
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Search completed: July 31, 2002, 09:21:41 Job time: 333 sec

376 NYVAIA 381

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Run on:
                                                                                                           OM protein - protein search, using sw model
July 31, 2002, 09:21:18; Search time 13.41 Seconds (without alignments) 1126.072 Million cell updates/sec
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Title: Perfect score: Sequence:

US-09-643-755B-2
2064
1 MNFLKSFPFYAFLCFGQYFV......REYYSVFDRANNLVGLAKAI 390

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 105224

105224 seqs, 38719550 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3322844333333028443333333333333333333333	. No.	Result
1108.5 1108.5 11094.5 11094.5 11084.5 11085.5	Score 1928)
33344444444444445555555555555555555555	3.4	
381 381 383 388 388 388 388 388 388 388	2 4	
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P18276 ovis aries O9912d2 callithrix Q9912d4 callithrix Q9912d5 callithrix Q9912d6 macaca fusc P1489 macaca fusc P297678 macaca fusc P28712 oryctolagus P28712 oryctolagus P27822 oryctolagus P27823 orycto	P00794 bos taurus	

45	44	43	42	41	40	39	38	37	36	35	34
668	670.5	675.5	691.5	699	718	728	744	747.5	772.5	775	784.5
32.4	32.5	32.7	33.5	33.9	34.8	35.3	36.0	36.2	37.4	37.5	38.0
419	400	402	365	387	345	382	380	389	390	407	410
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KDAP_MOUSE	RENI_SHEEP	RENI_RAT	CATD_SHEEP	ASPP_AEDAE	CATD_PIG	PAG1_SHEEP	PAG1_BOVIN	PAG1_PIG	CATD_BOVIN	CATD_RAT	CATD_MOUSE
0090	P521	P084	Q9mz	2031	P007	Q287	0294	. 0290	P80209	P242	P182
mus musculu	ovis aries	rattus norv	ovis aries	aedes aegyp	sus scrofa	ovis aries	bos taurus	sus scrofa	bos taurus	rattus norv	mus musculu

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[6] SEQUENCE FROM N.A. (CHYMOSIN A). SEQUENCE FROM N.A. (CHYMOSIN A). MEDLINE-83054629; PubMed-6183168; Moir D., Mao J., Schumm J.W., Vovis G.F., Alford B.L., Taunton-Rigby A.; Molecular cloning and characterization of double-stranded cDNA coding for bovine chymosin."; Gene 19:127-138(1982).	ACTIVE SITE PEPTIDES OF CHYMOSIN B. MEDLINE-75060332; PubMed-4612029; Chang WJ., Takahashi K.; "The structure and function of acid proteases. III. Isolation and characterization of the active-site peptides from bovine rennin."; J. Biochem. 76:467-474(1974).	SEQUENCE OF 17-77 (CHYMOSIN B). MEDLINE-76022411; PubMed-240697; Pedersen V.B., Foltmann B.; Panino-acid sequence of the peptide segment liberated during activation of prochymosin (prorennin)."; Bur. J. Biochem. 55:95-103(1975).	SEQUENCE OF 59-381 (CHYMOSIN B), AND DISULFIDE BONDS. MEDILINE-79239460; PubMed-381305; POLIMANN B., Pedersen V.B., Kauffman D., Wybrandt G.; "The primary structure of calf chymosin."; J. Biol. Chem. 254:8447-8456(1979).	SEQUENCE FROM N.A. (CHYMOSIN B). MEDLIND=82221400; PubMed=6283469; Harris T.J.R., Lowe P.A., Lyons A., Thomas P.G., Eaton M.A.W., Millican T.A., Patel T.P., Bose C.C., Carey N.H., Doel M.T.; "Molecular cloning and nucleotide sequence of cDNA coding for calf preprochymosin."; Nucleic Acids Res. 10:2177-2187(1982).	[1] SEQUENCE FROM N.A. (CHYMOSIN B). SEQUENCE FROM N.A. (CHYMOSIN B). MEDLINE-86301873; PubMed-3091454; Hidaka M., Sasaki K., Uozumi T., Beppu T.; "Cloning and structural analysis of the calf prochymosin gene."; Gene 43:197-203(1986).		P00794; 21-JUL-1986 (Rel. 01, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Chymosin precursor (EC 3.4.23.4) (Preprorennin). CYM OR CPC.	RESULT 1 CHYM_BOVIN STANDARD; PRT; 381 AA.

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PAR REPRESENTATION OF THE PROPERTY OF CONTROL OF THE PROPERTY 
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X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=92046065; PubMed=1942052;
Mewman M., Safro M., Frazao C., Kahn G.,
Blundell T.L., Andreeva N.;
"X-ray analyses of aspartic proteinases.
at 2.2-A resolution of bovine chymosin."
J. Mol. Biol. 221:1295-1309(1991).
                                                                    EMBL; M14077; AAA
EMBL; M14070; AAA
EMBL; M14071; AAA
EMBL; M14072; AAA
EMBL; M14073; AAA
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PIR; A00985; CMBO
PIR; A00985; CMBO
PIR; A20331; A256
PDB; ICMS; 15-UL
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MEROPS; A01.005;
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MEDLINE-91104895; PubMed-2271625;

Strop P., Sedlacek J., Stys J., Kaderabkova Z., Blaha I.,

Pavlickova L., Pohl J., Fabry M., Kostka V., Newman M., Frazao C.,

Shearer A., Tickle I.J., Blundell T.L.;

"Engineering enzyme subsite specificity: preparation, kinetic
characterization, and X-ray analysis at 2.0-A resolution of ValillPhe
site-mutated calf chymosin.";

Blochemistry 29:9863-9871(1990).
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MEDLINE=91017501; PubMed=2217166;
Gilliland G.L., Winborne E.L., Nachman
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MEDLINE=92412108; PubMed=1530626;
Huang K., Zhang Z., Liu N., Zhang Y., Zhang G., Yang K.;
"Functional implication of disulfide bond, Cys250 -Cys283, in
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InterPro; IPR001961; Pepsin.
Pfam; PF00026; asp; 1
PRINTS; PR00792; PEPSIN.
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A25631, A25631.
1CMS; 15-JUL-92.
3CMS; 15-OCT-92.
4CMS; 15-OCT-91.
1CZI; 01-APR-97.
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M14069; AAA30446.1;
M14070; AAA30446.1;
M14071; AAA30446.1;
M14072; AAA30446.1;
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MEDLINE-90356410; PubMed-2117748;
Pungecar J., Strukelj B., Gubensek F.,
"Complete primary structure of lamb prochua":
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CHYM_CALJA
ID CHYM_CALJA
ID CHYM_CALJA
AC Q9N2D2;
DT 16-OCT-2001
DT 16-OCT-2001
DT 01-MAR-2002
DE Chymosin pre
GN CYM.
OS Callithrix:
OC Enkaryota;
OC Mammalia; EN
OC Mammalia; EN
OC MAMMELITAXID=
CALLITATIAN.
AN
OX NCBI_TAXID=
RN [1]
RP SEQUENCE FR
RP SEQUENCE FR
RP REGULATION.
RC TISSUE-Gast
RA Kageyama T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 345
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ACT_SITE
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SEQUENCE
                                                                                                                                           Q9N2D2;
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
01-MAR-2002 (Rel. 41,
                                                                                                            Chymosin precursor CYM.
Callithrix jacchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zymogen;
SIGNAL
 TISSUE=Gastric mu
MEDLINE=20250834;
Kageyama T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; A01.006; ...
InterPro; IPR001166; Asp_protease.
InterPro; IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
                                                          NCBI_TaxID=9483;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00792; PEPSIN PROSITE; PS00141; ASP_PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Aspartyl
                                                                                                                                                                                                                                                                                          SQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPL 140
                                                                                                                                                                                                                                               NNLVGLAKAI
                                                                                                                                                                                                                                                                                                                                                 TVDSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                        SIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALSQGAEITRIPLYKGKPLRKALKERGLLEDFLQKQQYGVSSEYSGFGEVASVPLTNYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVTHAAEITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASVPLTNYLD
                                                                                                                                                                                                                                                                     NNLVGLAKAI
                                                                                                                                                                                                                                                                                                                                     TVDSVTISGAVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDSL
                                                                                                                                                                                                                                                                                                                                                                                                                            SIRYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P00794;
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                                            FROM
                                                                                       Eutheria;
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                                            Ν.Α.,
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                        mucosa
                                                                                                                                                                                          STANDARD;
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            PubMed=10788784
                                                                                       (Common marmoset),
; Chordata; Craniat
; Primates; Platyrı
                                                                                                                                   OH)
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                                            SEQUENCE
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93.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42074
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CHYMOSIN.
BY SIMILARITY.
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Pred. No. 1.9e
13; Mismatches
                                              엵
                                                                                      Craniata; Vertebrata; Euteleostomi; Platyrrhini; Callitrichidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Digestion;
                                             17-26,
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                                                                                                                                            on update)
                                                                                                                                                                                        381
                                              FUNCTION,
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l.9e-132;
nes 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                              AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  juice;
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Query Match
Best Local Similarity
Matches 301; Conser
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or send a
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB038386; BAA90873.1;
InterPro; IPR001969; Asp_pro
InterPro; IPR001461; Pepsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a clother the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: Hydrolyses a variety of proteins.
-!- CATALTYIC ACTIVITY: Broad specificity similar to clots milk by cleavage of a single bond in casein -!- ENZYME REGULATION: Inhibited by pepstatin.
-!- SUBUNIT: Monomer (By similarity).
-!- DEVELOPMENTAL STAGE: Expressed in adult, not neon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  evolution.";
J. Biochem. 127:761-770(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00026; asp; 1
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                            312
381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in other organisms.

MISCELLANEOUS: The optimal pH is around SIMILARITY: BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTIC ASPARTYL PROTEASES
                                          SYMPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDRA
                                                                                   SSMPTVVFEINGKKYPLPPSAYINQDQGFCTSGFQGDDSSQQWILGDVFIREYYSVFDRA
                                                                                                                                                           SIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASE
                                                                                                                                                                                                                                                                                SQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPL 140
                                                                                                                                                                                                                                                                                                                                                    AVTHAAEITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASVPLTNYLD 80
NNLVGLAKAI 390
                                                                                                                                              YSVPVFDNMMDRHLVAQDLFSVYMSRNEQGSMLTLGAIDPSYYTGSLHWIPVTVQEYWQF
                                                                                                                                                                                                                                                               CQYFGKIYIGTPPQEFTVVFDTGSSDLWVPSVYCNSVACQNHHRFDPSKSSTFQNMDKSL 131
                                                                                                                                                                                                                                                                                                                         ALSQASGIVRIPLHKGKSLRRALKERGLLEDFLKNHQHAVSRKHSNSREVASEFLTNYLD 71
                                                                                                                                                                                                       SIQYGTGSMQGLLGYDTVTVSSIVDPHQTVGLSTQEPGDVFTYSEFDGILGLAYPSLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s requires a license agreement (Si an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal
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59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16
58
381
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81.4%;
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Pepsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₩.
                                                                                                                                                                                                                                                                                                                                                                                 30;
                                                                                                                                                                                                                                                                                                                                                                                             Score 1605; DB 1;
Pred. No. 2.4e-115;
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BY SIMILARITY.
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C5820C74C97BB96B C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEPTIDE
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A1;
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                                                                                                                                                                                                                                                                                                                                                                                   39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 juice;
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MBL outstation -
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                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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16-OCT-2001 (Rel. 40,
01-MAR-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9N2D4;
                                                                                                                                                                                                                                          PROSITE; PS00141;
                                                                                                                                                                                                                                                       Pfam; PF00026; a PRINTS; PR00792;
                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kageyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Callithrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Callithrix jacchus (Common marmoset).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pepsin A precursor PGA.
                                                                                                                                                                                                                               Hydrolase;
                                                                                                                                                                                                                                                                          InterPro; IPR001969; Asp_protease
InterPro; IPR001461; Pepsin.
                                                                                                                                                                                                                                                                                                  EMBL; AB038384; BAA90871.1;
                                                                                                                                                                                                                                                                                                                                                                                 between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20250834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPA_CALJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372
18
                     30
                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Shows particularly broad specificity; involving phenylalanine and leucine are preferralso cleaved to some extent.

CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE PHE-, ENZYME REGULATION: Inhibited by pepstatin.

MISCELLANEOUS: The optimal pH is around 2.

SIMILARITY: BELONGS TO PEPFIDASE FAMILY AL; ALSO EUKARYOTIC ASPARTYL PROTEASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           World monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNLVGLAKAI 381
KVSLIKKKSLRKNLIEHGLLKDFLKNNTLDPASKYFPQGEAATMIANQPLVNYLDMEYFG
             RIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGE----VASVPLTNYLDSQYFG 85
                                            al Similarity
215; Conser
                                                                                                                                                                                                                    Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.,
                                                                                                                                                                                                                               Aspartyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127:761-770(2000)
                                                                                                               16
62
129
93
276
106
267
310
                                             Conservative
                                                                                                                                                                                                                                                                  asp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mucosa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                        PEPSIN
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of enzymatic
                                                                                                                                                                                                                                           ASP_PROTEASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10788784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             )
EC
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61
387
129
93
276
111
271
343
                                                                                                                                                                                                                               protease;
                                                                                                                                                                                                                                                                                                                                  license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                     41563
                                                       53.7%;
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Last annotation updat
C 3.4.23.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                     MW;
                                             49;
                                                                                                   ACTIVATION PEPTIDE (
PEPSIN A.
PHOSPHORYLATION (BY
BY SIMILARITY.
                                           Score 1108.5; DB Pred. No. 1.9e-77; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF.
                                                                                                                                                                                                                              E; 2.
Digestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A and C, and properties, (
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01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
Embryonic pepsinogen precursor (EC 3.4.23.-).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Archosauria; Aves; Neognathae; Galliformes; Phaslanidae;
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Hayashi K., Agata K., Mochii M., Yasugi S., Eguchi G.,
Molecular cloning and the nucleotide sequence of cDNA
chicken pepsinogen: phylogenetic relationship with pro
J. Biochem. 103:290-296(1988).
-I- DEVELOPMENTAL STAGE: SPECIFICALLY SECRETED DURING 1
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PROSITE; PS00141; ASP_PROTEASE; Digestion;
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MEDLINE=92037645; PubMed=1935977;
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NCBI_TaxID=9543;
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Pfam; PF00026; asp;
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InterPro; IPR001791;
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MY: 706F7ED50FF59COD CRC64;
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Pred. No. 3.2e
33; Mismatches
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hes 97;
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PGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-1988) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SHOWS PARTICULARLY BROAD SPECIFICITY; ALTH INVOLVING PHENYLALANINE AND LEUCINE ARE PREFERRED, MALSO CLEAVED TO SOME EXTENT.
-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE PHE-, LEU-
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY AL; ALSO KNC
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00141; ASP_PROTEASE; 2.
Hydrolase; Aspartyl protease; Digestion;
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InterPro; IPR001791; Lamin1n
InterPro; IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
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HSSP; P00790; 1PSN.
MEROPS; A01.001; -.
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                                    ITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASV----PLTNYLDSQY
IYKVPLVRKKSLRRNLSEHGLLKDFLKKHNRNPASKYFPQTEAPTLIDEQPLENYLDVEY
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, Zelle B., Bebelman J.P., Pr
Eriksson A.W., Frants R.R.;
sequencing of rhesus monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEMQAR.
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Catarrhini; Cercopithecidae;
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PHOSPHORYLATION
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23-OCT-1986 (Rel. C
01-AUG-1992 (Rel. 2
30-MAY-2000 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete amino acid sequence of mon J. Biol. Chem. 261:4395-4405(1986).
-!- FUNCTION: SHOWS PARTICULARLY BROAD SINVOLVING PHENYLALANINE AND LEUCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-81006790; PubMed=6773933; Kageyama T., Takahashi K.; "Monkey pepsinogens and pepsins. IV. Th activation peptide segment of Japanese J. Blochem. 88:9-16(1980).
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Eur. J. Biochem.
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Kageyama T., Takal
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MEDLINE=92037645; PubMed=1935977;
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Eukaryota; Metazoa; Chordata; Craniata; Va
Mammalia; Eutheria; Primates; Catarrhini;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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MISCELLANEOUS: EACH PEPSINOGEN IS CONVERTED TO CORRESPONDING PEPSIN AT PH 2.0 IN PART AS A RESULT OF THE RELEASE OF A 47 PEPSIN AT PH 2.0 IN PART AS A RESULT OF STEPWISE PROTECTION SEGMENT AND IN PART AS A RESULT OF STEPWISE PROTECTION OF THE PRO
                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE PHE-, LEU-. DEVELOPMENTAL STAGE: PREDOMINANT AT THE JUVENILE & ADULT STAGES MISCELLANEOUS: THE EXPRESSION OF PEPSINOGEN GENES IS REGULATED HORMONES AND RELATED SUBSTANCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                ALSO CLEAVED TO SOME EXTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RANNQVGLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385
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. 23, Last sequence upo
. 39, Last annotation of the contraction of the co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PROUVES, FACTOR PROSITE; PROOF PROSITE; PROOF PROSITE; PROOF PROSITE; PROTEASE; Digestion; Stomach; GHydrolase; Aspartyl protease; Digestion; Stomach; Grandon Phosphorylation; Multigene family; Signal.
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InterPro; IPR001791; Laminin_G.
InterPro; IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
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           RANNLVGLA
RANNQVGLA
                                                              MPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQS----ENHSQKWILGDVFIREYYSVFD
                                                                                                            DSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSY
                                                                                                                                                               PVFDNMMNRHLVAQDLFSVYMDRNGQE-SMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTV
                                                                                                                                                                                                              YGTGSMQGILGYDTYTVSNIYDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSI
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                                                                                                                                                                                                                                                              FGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIH 143
                                               LPDIVFTINGIQYPVPPSAYILQSQGSCTSGFQGMDVPTESGELWILGDVFIRQYFTVFD
                                                                                               DSITMNGEAIACAEGCQAIVDTGTSLLTGPTSPIANIQSDIGASENSDGEMVVSCSAISS
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pepsin A precursor (EC 3.4.23.1).
PGA3 AND PGA4 AND PGA5.
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MEDLINE=83161158; PubMed=6300126;
MEDANA F., Fujii-Kuriyama Y., Mizukami
Sogawa K., Fujii-Kuriyama pepsinogen
"Primary structure of human pepsinogen
J. Biol. Chem. 258:5306-5311(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [4]
SEQUENCE OF 16-100 (ISOZYMES 2; 3; 3A; 4 AND 5).
MEDLINE-90130402; PubMed=2515193;
Athauda S.B.P., Tanji M., Kageyama T., Takahashi K.;
Athauda S.B.P. arnji M., Kageyama T., Takahashi K.;
"A comparative study on the NH2-terminal amino acid sequences and armounties of six isozymic forms of human pepsinogens."
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Eukaryota; Metazoa;
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J. Biochem. 98:483-492(1985).
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-i- FUNCTION: SHOWS PARTICULARLY BROAD SINVOLVING PHENYLALANINE AND LEUCINE
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MEDLINE=86059312; PubMed=2415509;
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Fujinaga M., Chernaia M.M.,
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MEDLINE=89065108;
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SIMILARITY: BELONGS TO PEPTIDASE FAMI
EUKARYOTIC ASPARTYL PROTEASES FAMILY.
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NE-95392399; PubMed=7663352;
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M.J.V., Pronk J.C.,
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                                                                                     and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
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241:69-72(1988).
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C., Mager W.H.,
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Local Match

Similarity

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MEDLINE=92037645; PubMed=1935977;
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P27678;
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30-MAY-2000 (Rel. 39, Last annotation
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Tsukagoshi N. Ando Y., Tomita Y.
Sasaki T., Yamagata H., Udaka S.,
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InterPro; IPR001969; Asp_pro
InterPro; IPR001791; Laminin
InterPro; IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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PROSTITE: PSO01141; ASP_PROTEASE; 2.
Hydrolase; Aspartyl protease; Digestion; Stomach; Tymnogen; Multigene family; Signal; Glycoprotein.
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Tomita Y., Uchida R., Takemura
Udaka S., Ichihara Y., Takahasl
d expression in Escherichia col:
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"Isolation of human, swine, and rat prepepsinogens and calf preprochymosin, and determination of the primary structures NH2-terminal signal sequences.";
J. Blochem. 98:483-492(1985).
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MEDLINE=69054241; PubMed=4881358;

MEDLINE=69054241; PubMed=4881358;

Ong E.B., Perlmann G.E.;

"The amino-terminal sequence of porcine
J. Biol. Chem. 243:6104-6109(1968).
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SEQUENCE OF 16-134.
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PubMed=4584879;
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"Complete amino acid sequence of hog
"EBS Lett. 43:207-211(1974).
[3]
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                                                                                                                                                                                                                                                        structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bayliss R.S., Knowles J.R., Wybrandt G.E "An aspartic acid residue at the active and sequence of the heptapeptide."; Biochem. J. 113:377-386(1969).
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                                                                                                                                                                                                                                                            MEDLINE=90317821; pubMed=2115088;
Cooper J.B., Khan G., Taylor G., Tickle I.J., Blundell T.L.,
"X-ray analyses of aspartic proteinases. II. Three-dimensional
structure of the hexagonal crystal form of porcine pepsin at 2
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"Primary struc
                  MEDLINE=91278095; PubMed=2056534;
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                                                                                                                                                                                                                                                                                                                                                                                       "X-ray crystallographic studies of pepsin."; adv. Exp. Med. Biol. 95:23-31(1977).
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                                        -RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
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Sogawa K., Takahashi K.;
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A structure of po
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n. III. Amino acid sequence
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  James M.N.G.;
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MEDLINE=92279205; PubMed=1594574;
Hartsuck J.E., Koelsch G., Remington S.
"The high-resolution crystal structure
Proteins 13:1-25(1992).
-i- FUNCTION: SHOWS PARTICULARLY BROAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO PEPTIDASE FAMILY A EUKARYOTIC ASPARTYL PROTEASES FAMILY. DATABASE: NAME=Worthington enzyme manual;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMINO END.
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: PREFERENTIAL PTM: MINOR AMOUNTS OF THE ACTIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WWW="http://www.worthington-biochem.com/manual/P/PM.html"
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EMBL; M20920; AAA31095.1; -PIR; A00982; PEPG.
PIR; B22434; B22434.
PIR; JT0307; JT0307.
PDB; 3PEP; 15-APR-90.
PDB; 4PEP; 15-JAN-91.
PDB; 5PEP; 15-JUL-90.
PDB; 1PSA; 31-JAN-94.
PDB; 2PSG; 15-JAN-93.
MEROPS; A01.001; -PEROPS; A01.001; -PEROPS CHAIN
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InterPro; IPR001791; Laminin_G.
InterPro; IPR001461; Pepsin. STRAND :ymogen; PS00141; Signal; Aspartyl 166 1107 1177 1177 1104 2055 309 3119 1128 323 323 323 323 661 666 669 729 720 800 844 tyl protease; Digestion; Stomach; Phosphorylation; 3D-structure. ASP_PROTEASE; N -> D (IN REF. 3 AND DS -> SD (IN REF. 2).
Q -> E (IN REF. 2).
MISSING (IN REF. 2 AND S -> Q (IN REF. 5).
N -> D (IN REF. 5). PHOSPHORYLATION PEPSIN ACTIVATION PEPTIDE 2. (IN REF. 2). AND

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Pred. No. 1
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RESULT

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01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 39, Last annotation update)
30-Max-2000 (Rel. 39, Last annotation update)
Pepsin II-1 precursor (EC 3.4.23.1) (Pepsin A).
Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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HSSP; P00791; 1PSA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structure and development of rabbit
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Biol. Chem. 265:17031-17038(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: SHOWS PARTICULARLY BROAD SPECIFICITY; ALTHOUGH BONDS INVOLVING PHENYLALANINE AND LEUCINE ARE PREFERRED, MANY OTHERS ALSO CLEAVADD TO SOME EXTENT.

CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE PHE-, LEU-DEVELOPMENTAL STAGE: PEPSINOGENS IN GROUP I, II, AND III WHERE THE PREDOMINANT ZYMOGENS AT LATE POSTNATAL STAGE.

MISCELLANEOUS: THE EXPRESSION OF PEPSINOGEN GENES IS REGULATED HORMONES AND RELATED SUBSTANCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1; ALSO KNOWN EUKARYOTIC ASPARTYL PROTEASES FAMILY.
SVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYM
                                                                                                                                                                                                                                  VFDNMMNRHLVAQDLFSVYMDRNGQE-SMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTVD
                                                                                                                                                                            GTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSIP
                                                                                                                                                                                                                                                                                                                          VHKVPLVRKKSLRKNLIEKGLLQDYLKTHTPNLATKYFPKETFASVSTESLENYLDAEYF
                                                                                                                                                                                                                                                                                                                                                GTGSMTGILGYDTVKVGNIEDTNQIFGLSKTEPGITFLVAPFDGILGLAYPSISASDATP
                                                              VFDNMWNEGLVSEDLFSVYLSSNGEKGSMVMFGGIDSSYYTGSLNWVPVSHEGYWQITMD
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PS00141; ASP_PROTEASE;
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be K., Koiwai O.
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Pred. No. 1.4e
53; Mismatches
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01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pepsin II-4 precursor (EC 3.4.23.1) (Pepsin A).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutmanalla; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-91009127; PubMed-2129536;
Kageyama T., Tanabe K., Koiwai O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEP4_RABIT P28713;
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InterPro; IPR001461;
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                                                                                                                                                                                                             Zymogen;
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                                                                 Local Sir
hes 203;
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                                                                                                                                                                                                                                                                                                                                  ne expression during development.";
Biol. Chem. 265:17031-17038(1990).
- FUNCTION: SHOWS PARTICULARLY BROAD SPECIFICITY; A
INVOLVING PHENYLALANINE AND LEUCINE ARE PREFERREL
ALSO CLEAVED TO SOME EXTENT.
- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE PHE-, I
- DEVELOPMENTAL STAGE: PEPSINGENS IN GROUP I, II,
THE PREDOMINANT ZYMOGENS AT LATE POSTNATAL STAGE.
- MISCELLANEOUS: THE EXPRESSION OF PEPSINGEN GENES
                                                                                                                                                                                                                                                                                                       HORMONES AND RELATED SUBSTANCES.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1;
EUKARYOTIC ASPARTYL PROTEASES FAMILY.
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                                        ITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKY---SGFGEVASVPLTNYLDSQYF
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          GKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHY
                             VHKVPLVRKKSLRKNLIEKGLLQDYLKTHTPNPATKYFPKETFATVSTESLENYLDAEXF
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                                                                         Similarity
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 Aspartyl protease; Digestion; Stomach; Gastric
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                                                                                                                       ACTIVATION PEPTIDE.

PEESIN II-4.

PHOSPHORYLATION (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
                                                                Score 1037; D
Pred. No. 5.5e
57; Mismatches
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InterPro; IPR001969; Asp_protease.
InterPro; IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
PRINTS; PR00792; PEPSIN.
PROSTITE; PS00141; ASP_PROTEASE; 2.
Hydrolase; Asparttyl protease; Diges;
Zymogen; Signal; Phosphorylation; M
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01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pepsin III precursor (EC 3.4.23.1) (Pepsin
Oryctolagus cuniculus (Rabbit)
                                                                                                                                 modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/see/apressed.com/s
EMBL; M59237; PIR; E38302;
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEP3_RABIT
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                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                           м59237;
                                                                                                                         an email to license@isb-sib.ch).
   E38302.
                                              AAA85370.1;
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IN GROUP I, II,
POSTNATAL STAGE
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PEPSINOGEN GENES
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4PEP.

Digestion;

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Gastric juice;

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Best Local Similarity
Matches 199; Conserv
                                             Kageyama T., Tanabe K., Koiwai O.;

*Structure and development of rabbit pepsinogens. Stage-specific zymogens, nucleotide sequences of cDNAs, molecular evolution, and gene expression during development.";

J. Biol. Chem. 265:17031-17038(1990).

-I- FUNCTION: SHOWS PARTICULARLY BROAD SPECIFICITY; ALTHOUGH BONI INVOLVING PHENYLALANINE AND LEUCINE ARE PREFERRED, MANY OTHE:
ALSO CLEAVED TO SOME EXTENT.
                                                                                                                                                                                                      01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pepsin II-2/3 precursor (EC 3.4.23.1) (Pepsin A).
Oryctolagus cuniculus (Rabbit).
Dikaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9986;
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CHAIN
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SEQUENCE
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ALSO CLEAVED TO SOME EXTENT.
CATALYTIC ACTIVITY: PREFERENTIAL
DEVELOPMENTAL STAGE: PEPSINOGENS
THE PREDOMINANT ZYMOGENS AT LATE
MISCELLAMEOUS: THE EXPRESSION OF
HORMONES AND RELATED SUBSTANCES.
                                                                                                                                                                                                                                                                                                                                                                ANNLYGLAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYM
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PEPSIN III.
PHOSPHORYLATION (POTENTIAL).
BY SIMILARITY.
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Pred. No. 9.
                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                               Leporidae;
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                     L CLEAVAGE PHE-, L
S IN GROUP I, II,
E POSTNATAL STAGE.
             PEPSINOGEN GENES
                                                                                                                                                                                                                                                                                          387
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PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE;
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402	399	386	397	389	376	389	396	406	387	375	370	389	389	383	387	389	389	392	388	384	383	389	387	387	387	376	378	388
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057572	093458	Q9TTW8	Q28546	Q9MYK2	Q9TTX4	Q9мүкз	Q9D7T2	P70068	046496	046500	Q9TTW1	Q9W643	Q9PWK1	Q9DE45	Q9DDV5	Q9GMY3	Q9GMY4	Q9D7R7	Q9GMY2	Q91322	Q9DEC3	Q9GMY5	Q9JKE6	Q9D106	09ЛЛХ2	Q9PUR8	Q9PUR9	046523
	8	Q9ttw8 capra hircu	Q28546 ovis aries			sus s		8 pag	Sod	046500 bos taurus	bos tau	gallus			Q9ddv5 salvelinus	Q9gmy3 rhinolophus	Q9gmy4 sorex ungui	Q9d7r7 mus musculu	U	rana ca		S		Q9d106 mus musculu			Q9pur9 pseudopleur	046523 equus zebra

ALIGNMENTS

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RESULT ON INTERPRETATION OF THE PROPERTY OF TH
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                                                                                                                                                           Query Match
Best Local Similarity
Matches 357; Conserv
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Q9N1P5;
01-OCT-2000 (TIEMBLTel. 15, C.
01-OCT-2000 (TIEMBLTel. 15, L.
01-DEC-2001 (TIEMBLTEL. 19, L.
PROCHYMOSIN.
                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001969; Asp_protease.
InterPro; IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE; 2.
Aspartyl protease; Hydrolase.
SEQUENCE 366 AA; 40498 MW; 27981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Batish V.K., Mukhopadhyay U.K., Mohanty A.K., Grover S., Kuipers O.P.;
Submitted (AUG-199) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY AI; ALSO KNOWN AS THE
EUKARYOTIC ASPARTYL PROTEASES FAMILY.
EMBL; AF177290; AAF27315.1; --
HSSP; P00794; 4CMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bubalus bubalis (Domestic water buffalo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetarriodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bubalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=89462;
                                                                                   26
               N
AEITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASVPLTNYLDSQYFG 85
                                                                                                                                                               Conservative
                                                                                                                                                                                          91.2%;
97.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                       Score 1883; DB 6;
Pred. No. 5.7e-150;
3; Mismatches 5;
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                                                                                                                                                                                                                                  Length
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Q27951
ID 27951
ID 27
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                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 342; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996
01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q27951;
Q27951;
                                                                                                                                                                                                                                                                                                         Piam; pr00026; asp; 2.
Prints; pr00792; presin.
PROSITE; pr00141; Asp_protease;
SEQUENCE 345 AA; 38034 MW; ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-1995) to EMBL; U19786; AAA73476.1 HSSP; P00794; 4CMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Tan S.-y., Zhang Y.-y.,
"Nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001969; InterPro; IPR001461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; A01.006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA deletion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Bovinae; Bos. NCBI_TaxID=9909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos primigenius (aurochs).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROCHYMOSIN
  146
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                                                          KIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYG
                                                                                                                                                AEITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASVPLTNYLDSQYFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYMPT
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  TGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSIPV
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93.7%;
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Pepsin.
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01,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                           Score 1760.5; DB 6;
Pred. No. 1e-139;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                    396DECEE2996AlFA CRC64;
                                                                                                                                                                                                                                                                                                                                       UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345
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                                         DPRKSSTFQNLGKPLSIHYG
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NA and the m
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                                                                                                                                                                                          Query Match
Best Local Sin
Matches 309;
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Q9GK11;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CHYMOSIN PRECURSOR (EC 3.4.23.4).
Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
                                                                                                                                                                                                                                                 PROSITE: PS00141; ASP_PROTEASE: 1.
ASPARTY1 protease; Hydrolase; Signal.
SIGNAL 1 58 POTENTIA
CHAIN 59 381 CHYMOSIN
SEQUENCE 381 AA; 42082 MW; 24BADE
                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001969; Asp_protease
InterPro; IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=GASTRIC
                                                                                                                                                                                                                                                                                                                PRINTS; PR00792; PEPSIN.
                                                                                                                                                                                                                                                                                                                                                               MEROPS; A01.006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=GASTRIC MUCOSA;
Kappeler S.R., Farah Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Camel (Camelus dromedarius)
                                              131
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191
                      200
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|LAKAI 345
                                                                                                                                          LSIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLAS
                                                                                                       DSQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAKAI 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVFEINGKMYPLTPSAYTSQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDRANNLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYMPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYMPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FDNMMNRHLVAQDLFSYYMDRNGQESMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTVDSV
           EYSIPVFDNMMNRHLYAQDLFSVYMDRNGQESMLTLGAIDPSYYTGSLHWVPVTVQQYWQ
                                                                                             \tt DSQYFGKIYIGTPPQEFTVVFDTGSSDLWVPSIYCKSNVCKNHHRFDPRKSSTFRNLGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVFEINGKMYPLTPSAYTSQDQGFCTSGFQSENHSQKWILGDVFTREYYSVFDRANNLVG
EYSVPVFDNMMDRHLVARDLFSVYMDRNGQGSMLTLGAIDPSYYTGSLHWVPVTLQQYWQ
                                              LSIHYGTGSMEGFLGYDTVTVSNIVDPNQTVGLSTEQPGEVFTYSEFDGILGLAYPSLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FDNMMNRHLVAQDLLSVYMDRNGQESMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTVDSV
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                                                                                                                                                                                          Similarity 83.3
09; Conservative
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59
381
                                                                                                                                                                                                      80.9%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                        the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                              Puhan Z.;
ius) Chymosin
                                                                                                                                                                                          34;
                                                                                                                                                                                          Score 1670; D
Pred. No. 4.7e
34; Mismatches
                                                                                                                                                                                                                                                                 CHYMOSIN
                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                      24BADB57B2E7FDD7
                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                          ; DB 6;
1.7e-132;
hes 28;
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Best Local S
Matches 297
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SIGNAL
PROPEP
CHAIN
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Houen G., Madsen M.T., Harlow K.W., Loenblad P.,
"The primary structure and enzymic properties of
and chymosin.";
Int. J. Biochem. Cell Biol. 28:667-675(1996).
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Q28950;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00026; asp; 1. PRINTS; PR00792; PEPSIN.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U14406; AAB08492.1; HSSP; P00794; 4CMS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001969; InterPro; IPR001461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; A01.006;
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                      LSIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLAS
                                                                           LALSQGSGITRVPLRKGKSLRKELKERGLLEDFLQKQPYALSSKYSSFGEVASEPLTNYL
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380 AA;
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41771 MW;
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80.1%;
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                                                                                                                                                                                                                                                       Score 1601; DB 6; Pred. No. 2.9e-126;
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ACTIVATION PEPTIDE (POTENTIAL).
CHYMOSIN.
; ECA81B78239D2102 CRC64;
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Best Local Similarity
Matches 265; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
SEQUENCE
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O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROCHYMOSIN PRECURSOR (EC 3.4.23.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001969; Asp_protease.
InterPro; IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kageyama T., Ichinose M., Tsukada-Kato S., Omata M., Narit Moriyama A., Yonezawa S.;
"Molecular cloning of neonate/infant-specific pepsinogens stomach mucosa and their expressional change during develo Biochem. Biophys. Res. Commun. 267:806-812(2000).
EMBL; AJZ51688; CAB75983.1; -.
HSSP; P00794; 4CMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal; Hydrolase.
SIGNAL 1
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20139732; PubMed=10673373;
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                                       KYSVPIFDNMMNRHLVAQDLFSVYMSRNDQGSMLTLGAIDQSYFIGSLHWVPVTVQGYWQ
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                                                                                                                               LFVQYGTGSVEGFLAYDTVTVSDIVVPHQTVGLSTEEPGDIFTYSPFDGILGLAYPTFAS
                                                                                                                                                       LSIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLAS 199
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Rodentia;
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PROCHYMOSIN.
; 49F650CC759A5ADC CRC64;
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Sciurognathi; Muridae;
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; Murinae; Rat
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Best Loc
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01-NOV-1996
01-DEC-2001
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EMBL; J00004; AAA30449.1; -.
HSSP; P00794; 1CMS.
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TISSUE=FOURTH STOMACH MUCOSA;
MEDLINE=82189915; PubMed=6804449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
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Q9GMY6;
01-MAR-2001
                                             09GMY6
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"Nucleotide sequence of calf prorennin
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1es 237; Conservative
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; 26684 MW; '
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Pred. No. 6.7e-97;
2; Mismatches 3
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01-MAR-2001 (7
01-MAR-2001 (7
01-DEC-2001 (7
PEPSINOGEN A.
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PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE;
Aspartyl protease; Hydrolase.
SEQUENCE 386 AA; 41551 MW; 5
    Eukaryota;
Amphibia;
                                                                                                                                                                      Q9DEC4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (Dog).
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PGNA.
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                                           Rana catesbeiana (Bull frog).
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InterPro; IPR001791;
InterPro; IPR001461;
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VALSECA-IVKVPLVRKKSLRQNLIEHGLLNDFLKNQSPNPASKY--FPQEPTVLATQSL
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    Batrachia;
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tion of Insectivora in
                          Chordata;
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      Neobatrachia;
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Pred. No. 1.4e-84;
4; Mismatches 96
                          Craniata;
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    Vertebrata;
a; Ranoidea;
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      Ranidae;
                          Euteleostomi;
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"Molecular Cloning of
Rana catesbelana.";
Submitted (JUN-2000) t
                   SEQUENCE FROM N.A.

Narita Y., Oda S., Takenaka O., Kageyama T.;

"Phylogenetic position of Insectivora inferred of pepsinogen A and C.";
                                                                                                                       Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Insectivora;
MCBI_TaxID=9378;
                                                                                                                                                                Suncus murinus (House shrew) (Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                             PGNA
                                                                                                                                                                                                                              PEPSINOGEN A.
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InterPro; IPR001461; Pep
Pfam; PF00026; asp; 1.
PRINTS; PR00792; PEPSIN.
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47; Mismatches
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1; Craniata; Vert
7ora; Soricidae;
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                                                       "Phylogenetic position of Insectivora inferred f
of pepsinogen A and C.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ da
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1;
EUKARYOTIC ASPARTYL PROTEASES FAMILY.
EMBL; AB047244; BAB11750.1; -.
HSSP; P00790; 1PSN.
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01-MAR-2001 (TrEMBLrel.
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01-DEC-2001 (TrEMBLrel.
Pfam; PF00026;
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Eukaryota; Metazoa; Chordata; Craniata; Ver
Mammalia; Eutheria; Insectivora; Soricidae;
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PROSITS; PS00141; ASP_PROTEASE;
Aspartyl protease; Hydrolase.
SEQUENCE 387 AA; 41576 MW;
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EMBL; AB047243; BAB11749.1; -.
HSSP; P00790; 1PSN.
InterPro; IPR001969; Asp_protease.
InterPro; IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
                InterPro; IPR001969; Asp_protease
InterPro; IPR001461; Pepsin.
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57.1%;
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J. Biol. Chem. 264:4482-4489(1989).
T. SIMILARITY: BELONGS TO PEPTIDASE FAMILY.
EUKARYOTIC ASPARTYL PROTEASES FAMILY.
EMBL; J04601; AAA31096.1;
HSSP; P00791; LPSA.
MEROPS; A01.001; -
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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PROSITE;
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PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE;
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01-NOV-1996 (TrembLrel.
01-DEC-2001 (TrembLrel.
pepSINOGEN A PRECURSOR.
                                                                                                                                                           InterPro; IPR001969; Asp_protease
InterPro; IPR001791; Laminin_G.
                                                                                                                                        InterPro; IPR001461; Pepsin.
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Lin X.-L., Wong R.N.S., Tang J.;
"Synthesis, purification, and active-site mutagenesis
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41514 MW;
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of pepsinogen A and C.";

RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ data CC -: SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1; AL: CC EUKARYOTIC ASPARTYL PROTEASES FAMILY.

PR HSSP; P00790; 1PSN.

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PEPSINOGEN A
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PROSITE; PS00141, ASP_PROTEASE;
ASPARTLY1 Protease: Hydrolase.
SEQUENCE 386 AA; 41591 MW;
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4; Mismatches
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a; Microchiroptera; Rhinolophidae;
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                                                                                       Query Match 52.5%;
Best Local Similarity 55.2%;
Matches 207; Conservative 5
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC -2001 (TrEMBLrel. 19, Last annotation update)
01-DEC -PRECURSOR (EC 3.4.23.1)
Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus
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                                                                                                                                                                                                                                              InterPro; IPR001969; Asp_protease.
InterPro; IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE; 1.
Aspartyl protease; Hydrolase; Signal.
Aspartyl protease; Hydrolase; Signal.
SIGNAL 1 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1; ALSO KNEE EUKARYOTIC ASPARTYL PROTEASES FAMILY.
EMBL; AJ131678; CAC19555.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-GASTRIC MUCOSA;
Kappeler S.R., Farah Z
                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; A01.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for Camel Milk.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kappeler S.R., Farah Z., Puhan Z.;
"Camel (Camelus dromedarius) Chymosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Q9DEC2;
Q1-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1; ALSO KNU EUKARYOTIC ASPARTYL PROTEASES FAMILY. EMBL; AB045380; BAB20798.1; -. HSSP; P00790; 1PSN. MEROPS; A01.001; -.
                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00141; ASP_PROTEASE; Aspartyl protease; Hydrolase. SEQUENCE 384 AA; 41888 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001969; Asp
InterPro; IPR001461; Pep
Pfam; PF00026; asp; 1.
PRINTS; PR00792; PEPSIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rana catesbeiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ikuzawa M., Inokucn
"Molecular Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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  136
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hes 201;
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                     GSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEEPDGILGMAYPSLASEYSIPVF
                                                                                                                                                                              GSMSGFLGYDTLQVGNIQISNQMFGLSESEPGSFLYYSPFDGILGLAFPSIASSQATPVF
                                                                                  IYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYGT
                                                                                                                                                                                                        ITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKY-SGFGEVASVPLTNYLDSQYFGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QYWQFTVDSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISSSGGTPVFDNIWDEGLISEDLFSVYLSSNDESGSVVIFGGIDSSYYTGSLNWVPVSVE
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                                                                                                                                                                                                                                                                        Similarity 54.9
01; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inokuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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psinogens in A
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                                                                                                                                                                                                                                                                      Score 1081; D
Pred. No. 1.4e
64; Mismatches
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                                                                                                                                                                                                                                                                        ; DB 13;
1.4e-82;
hes 95;
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01-MAY-2000
01-DEC-2001
                                                                                                                                                                                                                                                                    CPGA.
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Sakamoto N., Yasugi S.; Submitted (MAR-1999) to
                                                                                                                                                                                                              Pfam; PF00026; asp; 1.
PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE; 2.
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=98440813; PubMed=9753645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEPSINOGEN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9PRG9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9PRG9
                                                                                                                                                                                        Aspartyl protease; Hydrolase.
SEQUENCE 382 AA; 42056 MW; C3C7EB8CA4DD3E28 CRC64;
                                                                                                                                                                                                                                               InterPro; IPR001969; InterPro; IPR001461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
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TGSMQGILGYDTVTVSNIVDIQ-QTVGLSTQEPGDVFTYAEFDGILGAAYPSLASEYSIP
TGSMSGILGYDTVAVSSI-DVQNQIFGLSETEPGSFFYYCNFDGILGLAFPSISSSGATP
                                                                                                   ITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGF--GEVASVPLTNYLDSQYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVFEINGKMYPLTPSAYTSQDQGFCTSGFQS----ENHSQKWILGDVFIREYYSVFDRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNMMNRHLVAQDLFSYYMDRNGQE-SMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTVDSV
||| :- |: |:|||| :- |: | :| ||:||:||: || ||:||
DNMWSQGLIPQNLFSVYLSSDGQTGSYYLFGGVDNSYYSGSLNWVPLTAETYWQITLDSV
                                             TISIGTPQQDFTVIFDTGSSNLWVPSIYCKSSACSNHKRFDPSKSSTYVSTNETVYIAYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVFTINGVQYPLSPSAYVRQNQQGCSSGFQAMNLPTNSGDLWILGDVFIRQYFTVFDRAN
                                                        KIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYG 145
                                                                                       IHRVPLKKGKSLRKQLKDHGLLEDFLKKHPYNPASKYHPVLTATESYEPMTNYMDASYYG
                                                                                                                                    201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                             49.2%;
                                                                                                                                                                                                                                               Asp_protease.
Pepsin.
                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
                                                                                                                                    57;
                                                                                                                                  Score 1016.5; DB 13; Length 382; 
Pred. No. 3.6e-77; 
7; Mismatches 97; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Вb
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                                                   PTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQS----ENHSQKWILGDVFIREYYSVFDR 379
                                                                                                                       ANNLYGLA 387
                                                                                           SVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYM 323
ANNKVGLS
                                        PDVTFHINGHAFTLPASAYVLNEDGSCMLGFENMGTPTELGEQWILGDVFIREYYVIFDR
                                                                                 RVTVGNKYVACFFTCQAIVDTGTSLLVMPQGAYNRIIKDLGVSSD--GE--ISCDDISKL
379
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Search completed: July 31, 2002, 09:24:51 Job time: 233 sec

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Result
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Copyright (c) 1993 - 2000 Compugen
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ALIGNMENTS

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DEFINITION
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SOURCE
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AX088021
LOCUS
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                                                                                                                                                                               REFERENCE
                                                                                                                                   AUTHORS
TITLE
JOURNAL
                                                                                          source
                                                                                                   van Rooijen,G., Keon,R.G., Boothe,J.
Commercial production of chymosin in
Patent: Wo 0114571-A 3 01-MAR-2001;
SemBioSys Genetics Inc. (CA)
Location/Qualifiers
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AX088021
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1554. 2726
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YPLTPSAYTSQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDRANNLVGLAKAI"
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1920	GCCTGCAAGAA	1861	Db
	ttcctctgacttctgggttccctctatctactgcaagagcaatgcctgcaagaaccac	1861	Qy
	TTTGGGAAGATCTACCTCGGAACCCCGCCTCAAGAGTTCACCGTTCTCTTTGATACT	1801	Дb
1860	ctttgg	1801	Qy
	TACCAACTACCTTGATAGTCAA		Db
1800	gtactccggcttcggtgaagttgctagcgtgccacttacca	1741	Qy
1740	GGACTTCTAGAAGACTTCTTGCAGAAACAACAGTATGGCATCAGCAGC		Db
1740	gaaggaacatggacttctagaagacttctt	σ	Qy
1680	CACCCGCATTCCTCTACAAAGGTAAGTCTCTCCGTAAGGCG	1621	Db
1680	tcacgctgctgagatcacccgcattcctctctacaa	6	Qy
1620	TTCTACGCTTTCCTTTGTTTCGGTCAATACTTCGTTGCTGT	1561	Db
1620	cttaagtctttccctttctacgctttcctttgttt	Ü	Qy
1560	CCCCAACCCATATTCAATACTACTCTACTATGA	1501	Db
1560	tactctactactataataccccaaccca	ū	Qy
1500	CTAATATCACTCACTTCTTTCATCCATCCATCCATCCAGAGTAC	4	Db
1500	acctataaatacctctaatatcactcacttctttc	1441	Qy
1440	GCCCAAATCTCCATGCATGTTCCAACCACCTTCTCTTATATA	w	Дb
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1140	AAAAGACAAAACAGAGAG	0	Db
1140	tgcatggftcttgcgcaagaaaaagacaaagaacaaagaaaaaaga	0	Qy
1080	GGCACTCTGTGGTCTTTTGGTT	1021	DЪ
1080	tgtaagtccgtaactagaattacagtgggttgccatggcact	1021	Qy
1020	TTTACCTTTTCTTGG	961	Db
1020	ataacatttatggtggactaattttcatattttcttattgcttttac	961	Qy
960		•	Db ·
960	tttaaaqtaaatataaqtaatqtaqtaqaqtqttaqaqtgttaccctaaaccataaac	01	ΟV
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900	attgttgaatttgtgactattgatttattattctactatgtttaaaattgttttatagat	841	Qy

3060	caattctaactttagcattgtgaacgagacataagtgttaagaagacataacaattataa 3 	y 3001	δ
3000	acggcttatggaatgcttcaaatagtacaaaaacaaatgtgtactataagactttctaaa 3 	y 2941 b 2941	유 양
2940 2940	tatgcaccttattgttctatgataaatttcctcttattattataaatcatctgaatcgtg 2	y 2881 b 2881	β δ
2880	gctccatctcacttcttctatgaataaacaaaggatgttatgatatattaacactctatc 2	y 2821 b 2821	유왕
2820 2820	gtaagagctcatggagagcatggaatattgtatccgaccatgtaacagtataataactga 2	y 2761 b 2761	å ö
2760 2760	tc9ttg9gctagctaaagcaatctgaagcttaataagtatgaactaaaatgcatgtaggt : 	270 270	β δ
2700 2700	ggatcttgggagatgtgttcattcgtgagtactacagcgtctttgacagggccaacaacc :	y 2641 b 2641	ρ δ
2640 2640	ccagccaggatcaagggttctgcaccagtggattccagagtgagaaccattcccagaaat;	y 2581 b 2581	ρ γ
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2460 2460	ataccggtacgtccaagctggtcggacctagcagcgacattctcaacattcagcaagcta;	y 2401 b 2401	B 8
2400	acagtgtcaccatcagcggtgtggttgttgcatgtgaaggtggatgtcaagctatcttgg;	y 2341 b 2341	B 6
2340 2340	acacaggatctcttcactgggttccagtcactgtgcagcagtactggcaattcactgtgg;	y 2281 b 2281	요 성
2280 2280	acatggacaggaatggccaggagagcatgctcacgcttggagctattgatccatcc	y 2221 b 2221	B 8
2220 2220	tacctgtgttttgacaacatgatgaaccgacacctagtagctcaagacttgttctcggttt :	y 2161 b 2161	유 &
2160 2160	atgcagaattcgatggcatccttggtatggcatacccatcgctcgc	y 2101 b 2101	β Q
2100 2100	ttgtggacattcaacagacagtaggacttagcacccaagaaccaggtgatgtcttcacct :	y 2041 b 2041	දු දි
2040 2040	actacggtacaggtagcatgcaaggaatcttaggctatgataccgtcactgtctccaaca:	Qy 1981 Db 1981	B 8
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Phaseolus vulgaris. Phaseolus vulgaris PHYBCSP 3502 bp DNA linear PLN 17-JUN-1998 Phaseolis vulgaris beta-type phaseolin storage protein gene, complete cds. J01263 M13758 J01263.1 GI:3228361

RESULT 2
PHVBCSP
LOCUS
DEFINITION

01 aacccttatacaaaaccccaaaaaccagtttcctagcaccctaccaactaaggtacc 3	390	Qy
	384	β δ
	37	뫄
 AGGCAAGGGAAATTTTTTAATTTGGGTTGTTTGTTTGCTGCATAATTTATGCAGTA Cactacacataaccctttttaqcaqtaqaqcaattqqttqaccqtqtqcttacttctt 	378	ο _ν Β
	37	ν
31 GTCCCAATCCTTATACAACCAACTTCCACAGGAAGGTCAGGTCGGGACAACAAAAAAAA	366	рb
) gtcccaatccttatacaaccaacttccacaggaaggtcaggtcgg	366	γQ
)1 ATGAAATTTTTTTTTTTTATCGGCAAGGAAATAAAATTAAATTAGGAGGGACAATGGTG	360	Db
tyaaattttttttttttatcyycaayyaaataaaattaaattaggagggacaatg	36	δŌ
TAAACGAGAGTAAACATATTTGACTTTTTGGTTATTTAACAATTATTTAT	354	ф
1 taaacgagagtaaacatatttgactttttggttatttaacaaattattatttaacact	354	γQ
31 AGTAAATAFTGTCATAAATCTATACAATCGTTTAGCCTTGCTGGACGACTCTCAATTATT	348	Дb
l agtaaatattgtcataaatctatacaatcgtttagccttgctggacgactctcaatta	348	Qy
21 ATAAATAACATATAATATATGTATATAAATTTATTATAATATAACATTTATCTATAAAA	34	ф
taaataacatataatatatgtatataaatttattataataatataacatttatctataaa	34	Qy
51 AAAAAAAAATTATGAGTTGGTTTGATAAAATATTGAAGGATTTAAAATAAT	336	DЬ
aaaaaaaaattatgagttggtttgataaaatattgaaggatttaaaataat	ω ω	Qy
01 TGTATAAAGGTTGGATCATCCTTAAAGTGGGTCTATTTAATTTTATTGCTTCTTACAGA	ω ω	ДЬ
gtataaaggttggatcatccttaaagtgggtctatttaattttattgcttcttacag	33	νo
`i >> ~	324	Дb
	32	Qγ
1 TACCCAT	318	ДD
acccatttatatattattatacttatccacttatttaatgtctttataaggtttgatcca	31	Qy
21 TGTTAAGGAGACATAACAATTATAAAGAGAGAAGTTTGTATCCATTTATATATA	31	рb
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61 TGGAAGAAGTTTGTCTCCATTTATATATATATATATATACCCACTTATGTATTATATATA	30	Дb
ggaagaagtttgtctccatttatatattattattattacccacttatgtattatatta	30	Qγ
01 CAATTCTAACTTTAGCATTGTGAACGAGACATAAGTGTTAAGAAGACATAACAATTATAA		מע

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Proc. Natl. Acad. Sci. U.S.A.
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                                  ccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacatcttctaa
                                                    gtagaaagcataaagatttattcttattcttcttcatataaatgtttaatatacaatata
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Rosidae; euros...

Phaseolus.

1 (sites)

RS Angenon,G., de Jaeger,G., Goossens,A. and De
RS Interuniversitair Instituut voor Bic
Location/Qualifiers
1...1415
1...1415
2985
                                              cal Similarity 99.6
1367; Conservative
aattoattgtactcccagtatcattatagtgaaagttttggctctctcgccggtggtttt
                                                                                                                                            /organism="Phaseolus
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a 259 c 172 g
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                                            Score 1353.6; DB 6;
Pred. No. 4.3e-204;
); Mismatches 4;
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RESULT 4
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Sequence
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Eukaryota;
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Commercial production of chymostin in
Patent: WO 0114571-A 1 01-MAR-2001;
SemBioSys Genetics Inc. (CA)
                                                                                                                                                                                                               Mammalia; Eutheria
Bovidae; Bovinae;
1 (bases 1 to 11)
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          299
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LFSVYMDRNGQESMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTVDSVTISGVVVACEG
GCQAILDTGTSKLVGPSSDILMIQQAIGATQNQYGEFDIDCDNLSYMFTVVFEINGKM
YPLTPSAYTSQDQGFCTSGFQSEMHSQKWILGDVFIREYYSVFDRANNLVGLAKAI"
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/db_xref="taxon:9913"
1. .1173
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                                                                                                                                                                                                                                 Eutheria;
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          agctacatgcctacagttgtcttttgagatcaacggcaagatgtacccactgaccccctcc
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2093 480 2033 420 180

1554 atgaacttccttaagtctttccctttctacgctttcctttgtttcggtcaatacttcgtt DB 6; L.3e-175; 0; Length Indels 0; Gaps 1613 0;

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Sequence 2 1
AX252300
AX252300.1
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Hypoallergenic transgenic soybeans
Patent: WO 0168887-A 2 20-SEP-2001;
E. I. du Pont de Nemours and Company
INTERNATIONAL, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthetic construct artificial sequence.
1 (bases 1 to 2970)
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nilarity 99.0%;
Conservative
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/db_xref="taxon:32630"
/note="chimeric construct"
/note="chimeric 527 g 878 t
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Patent W00168887
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Pred. No. 5.4e-172;
0; Mismatches 12;
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                                                                                                                                  BOVCHYMOB
bovine chymosin b (renn
J00003
J00003.1 GI:162859
chymosin; chymosin B; p
bovine (calf) cdna of f
Bos taurus
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                                                   Harris,T.J.R., Lowe,P.A., Lyons,A., Thomas,P.G., Eaton,M.A.W., Millican,T.A., Patel,T.P., Bose,C.C., Carey,N.H. and Doel,M.T. molecular cloning and nucleotide sequence of cdna coding for calf
chymosin is the major proteolytic enzyme in the unweaned calf. two chromatographically
                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
                       82221400
                                 preprochymosin
Nucleic Acids Res. 10,
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fourth stomach mucosa
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cagagtactcgatacctgtgtttgacaacatgatgaaccgacacctagtagctcaagact
                                                     GCAAAAACCACCAGCGCTTCGACCCGAGAAAGTCGTCCACCTTCCAGAACCTGGGCAAGC
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Location/Qualifiers
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/db_xref_"GI:162860"
/db_xref_"GI:162860"
/translation="mrclvvllavfalsogaeitriplykgkslrkalkehglledfl
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/translation="mrclvvllavfalsogaeitriplykgkslrkalkehglledfl
/translation="mkclvvvllsogaeitrifytegrefytriplgssdfwyps
IYCKSNACKNHOREDFRKSSTFONLGKPLSIHYGTGSNOGILCXDTYTYSUNIVDIOOT
VGLSTOEPGDVFTYAEFDGILGMAYPSLASEYSIPVFDNMMNRHLVAQDLFSVYMDRN
GQESMLTLGALNPSYYTGSLHWYPVTVQOYWOFTVDSVTISGYVVVACEGGCQAILDTG
TSKLVGPSSDILNIOQAIGATONOYGEFDIDCDNLSYMPTVVEEINGKMYPLTPSAYT
SQDOGFCTSGFOSENHSQKWILGDVFIREYYSVFDRANNLVGLAKAI"
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/db_xref="taxon:9913"
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/note="preprochymosin
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ee bovchymoa, bovchymoc). this sequence has tentatively
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Pred. No. 1.2e-132;
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                                      GGGCCAACAACCTCGTGGGGCCTGGCCAAAGCCATCTGA
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TGAGGAAGCGCTGAAGGAGCATGGGCTTCTGGAGGACTTCCTGCAGAAACAGCAGTATG
          tocgtaaggcgctgaaggaacatggacttctagaagacttcttgcagaaacaacagtatg
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Sequence
AR002347
                                                                                                                                                                               Kato,E.K. and Stuart,W.Dorsey
Light-regulated promoters for
in filamentous fungi
Patent: US 5741665-A 2 21-APR-
                                                                                                                                                                                                                                 Unclassified
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Pred. No. 3.7e-132;
0; Mismatches 141;
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TEIRAA MOIAA,
PI ARISON TAUNTON RIGUBII, JIERARUDO FURANSHISU BUOBUISU PC
C12N1/20, C07G7/00,C07H21/04,C12N15/00,C12P21/00//C12N1/18, PC
C12N1/20, PC
C12P19/34,C12R1/19,C12R1/865;
CC
C12N1/20, PC
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PD 01-SEP-1982
PF 14-JAN-1982 JP 1982003556
PR 16-JAN-1981 US 81 225717, 01-DEC-
ttgatagtcaatactttgggaagatctacctcggaaccccgcctcaagagttcaccgttc 1848
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Jierarudo,F.B. .
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14-JAN-1982 JP 1982003556
16-JAN-1981 US 81 225717,
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/organism="unidentified"
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Pred. No. 3.9e-132;
0; Mismatches 138;
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Bos taurus

Bokaryota; Metazoa; Chor

Boxidae; Eutheria; Ceta

Bovidae; Bovinae; Bos.

1 (bases 1 to 1291)

Simons, A. F. M. and De Vos
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                     Pecora;
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         aagctatcttggataccggtacgtccaagctggtcggacctagcagcgacattctcaaca
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Patent: EP 0307011-A 5 15-MAR-1989;
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S Moloney.M.M.

Preparation of heterologous proteins on Preparation of heterologous proteins on Location/Qualifiers

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"~~ism="unknown"
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104058
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                                activity
Patent: F
                                                                                           104058
Sequence !
104058
104058.1
                                                                       Unknown
                                                   1 (bases 1 to 1175)
Cashion, L.M., McCaman, M.T.,
                                            Recombinant DNA coding
                                                                 Unclassified.
                                                                              Unknown.
      263
                  EP 0123928-A2 5 07-NOV-1984;
Location/Qualifiers
1. .1175
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    /organism="unknown"
356 c 318 g
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                                            polypeptide
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attcccagaaatggatcttgggagatgtgttcattcgtgagtactacagcgtctttgaca
                         CCTCCGCCTATACCAGCCAAGACCAGGGCTTCTGTACCAGTGGCTTCCAGAGTGAAAATC
                                                         aagctatcttggataccggtacgtccaagctggtcggacctagcagcgacattctcaaca
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                                  tgatagtcaatactttgggaagatctacctcggaaccccgcctcaagagttcaccgttct
                                                                                                                                                                                                                                                                                                               GAGGAAGGCGCTGAAGGAGCATGGGCTTCTGGAGGACTTCCTGCAGAAACAGCAGTATGG
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AGAGTACTCGATACCCGTGTTTGACAACATGATGAACAGGCACCTGGTGGCCCAAGACCT
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Sequence
108097
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1 (bases 1 to 2726)

1 (bases 1 to 2726)

van den Berg, J.A.D. and Brake, A.J.D.

DNA constructs containing a Kluyveromyces alpha-factor leader sequence for directing secretion of heterologous derivatives Patent: EP 0301669-A1 5 01-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                          h 22.6%;
Similarity 82.7%;
24; Conservative
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Pred. No. 6.6e-132;
0; Mismatches 214;
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BOVCHYMOA
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coding for bovine chymosen gene 19, 127-138 (1982) 83054629 (rennin) is the major proteolytic enzyme in the fourth stomach of the unweaned calf. two chromatographically distinct forms are known and a third seems likely (see bovchymob and bovchymoc); this sequence has been tentatively identified as chymosin a; it differs from chymosin by only two amino acids from chymosin c by another amino acid. [1] argues that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ataataactgagctccatctcacttcttctatgaataa
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J00002
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                                                                                                                                                                                             Bovidae; Bovinae; Bos. 1 (bases 1 to 1275)
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Cetartioda
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chymosin; chymosin A; rennin.
bovlne (calf) cdna of fourth stomach
Bos taurus
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a (rennin) mrna
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                              variants of a single
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QKQQYGISSKYSGFGEVASVPITNYLDSQYFGKIYLGTPPQEETVLFDTGSSDFWVPS

IYCKSNACKNHQREDPRKSSTFQNIKGKPLSIIYGTGSKQFICYDTVTVSNIIDIQQI

YGKSTQEPGDVFTYAEEDGILGMAYPSLASEYSIPVEDNMMRHLVAQDLFSYYMDRN

GQESMLTLGAIDPCYYTGSLHWVPVTVQQYWQFTVDSVTISGVVVACEGGCQAILDTG

TSKLVGPSSDILNIQQAIGATQNQYDEFDIDCDNLSYMPTVVFEINGKMYPLTPSAYT
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/db_xref="taxon:9913"
21. .1166
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/db_xref="GI:162858"
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195. .1163
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Pred. No. 1.3e-131;
0; Mismatches 140;
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PRODUCTION OF POLYPEPTIDE
PRODUCTION OF POLYPEPTIDE
CELLTECH LTD
OS bovine
PN JP 1983009687-A/1
PD 20-JAN-1983
PF 17-JUN-1982 JP 1982104672
PR 17-JUN-1982 JP 1982104672
PR 17-JUN-1981 GB 81 8118688, 11-NOV-1981 GB 81
PR 17-JUN-1981 GB 81 8136185, 10-FEB-1982 GB 82 820390;
NOOMAN HENRI KEARI, MAIKERU TERENSU DOORU,
PI CHIMOSHII JIYON ROI HARISU,
PI C12N9/52_C07H21/04,C12N1/00,C12N9/60,C12N15/00, PC
C12R1/865;
CC strandedness: Double;
CC topology: Linear;
CC topology: Linear;
CC *source: tissue_type=stomach;
CC *source: tissue_type=stomach;
CC *source: clone=pCT 70;
FH Key Location/Qualifiers
FH S'UTR
FT sig_peptide 26..73
FT mat_peptide 74..1078
FT sig_peptide 74..1078
FT 3'UTR 1082..1200
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CDNA encoding chymc

E00075.1 GI:21683:

JP 1983009687-A/1.
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Bos taurus
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1 (bases 1 to 1290)
Nooman, H.K., Maikeru, T.D.,
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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TCCAGCAGGCCATTGGAGCCACACAGAACCAGTACGGTGAGTTTGACATCGACTGCGACA
            ttcagcaagctattggagccacacagaaccagtacggtgagttttgacatagattgcgaca
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/product='pre-pro-chymosin'
Location/Qualifiers
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/organism="Bos taurus"
/db_xref="taxon:9913"
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pred. No. 1.3e-131;
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Carey, N. H., Doel, M. T., Harris, T. J. R., A process for the production of a poly Patent: EP 0068691-A 29 05-JAN-1983;
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Search completed: July 31, 2002, 18:19:33

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Sequence encoding	. Chymosin open read	Cloned sequence of	Kunitz soybean try	Bovine pre-pro-chy	Nucleotide sequenc	Phaseolus vulgaris	Nucleotide sequenc	Bovine phaseolin p	Description

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Sequence encoding Sequence of proren BamHI insert from Prochymosin (prore Gene encoding (pre Gene encoding (pre Optimised prochymo Human stomach cell Human ovarian tumo Bovine pregnancy a Bovine pregnancy a Bovine pregnancy a Bovine pregnancy a Human aspartyl pro Gastric cancer ass Drosophila melanog DNA fragment of pA Bovine pregnancy a	Sequence of recomb Rennin gene. Synt 2.7 Kbp HindIII fr Sequence of prochy Pre-prorennin-A ge BamHI/Sall insert Sequence of prepro cDNA sequence corr Sequence of veal c

ALIGNMENTS

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RESULT
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                         AAS00570;
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(first entry)
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Bovine phaseolin promoter pre-pro-chymosin-phaseolin terminator.

Chymosin; transcription regulator; terminator sequence; soybean; corn; pre-pro-chymosin; rape seed; sunflower; cotton; tobacco; alfalfa; wheat; barley; oats; sorghum; Arabidopsis thaliana; potato; flax; linseed; rice; safflower; oil palm; ground nut; Brazil nut; coconut; castor; coriander; squash; jojoba; ds; phaseolin; promoter; terminator; mutant; French bean

Key promoter Chimeric - Bos sp. Chimeric - Phaseolus vulgaris. Location/Qualifiers /*tag=

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                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents a chimeric polynucleotide comprising a pre-pro-chymosin, a phaseolin promoter and a phaseolin terminator. Chymosin can be produced in a plant seed through introduction of a chimeric nucleic acid molecule, comprising a nucleic acid sequence encoding a chymosin polypeptide operatively linked to transcription regulator and terminator sequences, into a plant cell. The sequences are useful for producing plant seeds, in particular seeds of soybean, rape seed, sunflower, cotton, corn, tobacco, alfalfa, wheat, barley, oats, sorghum, Arabidopsis thaliana, potato, flax/linseed, safflower, oil pal groundnut, Brazil nut, coconut, castor, coriander, squash, jojoba and
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                                                                                             The present sequence represents the bean phaseolin promoter, which is used to construct plasmids for the expression of the P. putidated fands gene. The gene encodes an enzyme that may be used in the method of the invention. The specification describes a method for manipulating the metabolism of a plant, and comprises expressing a heterologous gene encoding fatty acid oxidation enzymes in the cytosol or plastids other than the peroxisomes, glyoxisomes or mitochondria of the plant. The method may be used to enhance the biological production of polyhydroxyalkanoates or novel oil compositions in a transgenic plant. Plants which may be used to produce these compounds in this way include Brassicas, maize, soybean, cottonseed, sunflower, palm, coconut, safflower, peanut, mustards, flax, tobacco and alfalfa. The method may also be used to prevent or suppress seed production and therefore increase the production of biomass (leaves,
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transgenic plant; prom
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                                                                                                                                                                                                 AAZ10392 standard;
                                                                                              WO9945122-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 901
                                   (META-)
                                                                 05-MAR-1999;
                                                                                10-SEP-1999
                                                                                                                          transgenic
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                                                                                                                                                                                                                                                                                                                         cgcaatcacacacccaactcaaattagtcactggctgatcaagatcgccgcgtccatgta
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                                                                                                                                                                                                                                           gtcatcccatgcccaaatctccatgcatgttccaaccaccttctctttatataatacct
                                                                                                                                                                                                                                                                                                                                                                                                                                           tgggtcttgcgcaagaaaaagacaaagaacaaagaaaaaaagacaaaacagagagacaaaa
 1999-540850/45
                                                                                                                                                                                                                                     ataaatacctctaatatcactcacttctttcatcatccatccatccagagtactactact
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                    L,
                                   METABOLIX INC
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                      Huisman
                                                   98US-0077107
                                                                 99WO-US04999
                                                                                                                           terminator;
                                                                                                                                                                                                  DNA;
                                                                                                                                                                    entry)
                      GW,
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                      Moloney
                                                                                                                                                      bean
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                                                                                                                           bean;
                                                                                                                                                      phaseolin
                      ĭ
                      Patterson
                                                                                                                                 oxidation enzyme;
seed production;
                                                                                                                                                       terminator
                      'n
                      Peoples
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                                                                                                                                  plant
                                                                                                                                   biomass;
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Modifying fatty biomass and prod producing specific poly n in plants, useful polymers in seeds for increasing

Example Ψ Page 79pp; English.

CC The present sequence represents the bean phaseolin terminator, which CC is used to construct plasmids for the expression of the P. putida CC faoAB gene. The gene encodes an enzyme that may be used in the CC method of the invention. The specification describes a method for CC manipulating the metabolism of a plant, and comprises expressing a CC heterologous gene encoding fatty acid oxidation enzymes in the CC cytosol or plastids other than the peroxisomes, glyoxisomes or CC mitochondria of the plant. The method may be used to enhance the CC biological production of polyhydroxyalkanoates or novel oil compositions CC compounds in this way include Brassicas, maize, soybean, cottonseed, CC sunflower, palm, coconut, safflower, peanut, mustards, flax, tobacco and CC alfalfa. The method may also be used to prevent or suppress seed CC production and therefore increase the production of biomass (leaves, XX stalks) by plants.

Sequence 1244 BP; 456 A; 174 ე 178 <u>.</u> 436 ;; 0 other

δÃ Вb Qy В Qγ DЬ Qy DЬ Qγ 밁 ρy В Qγ В Ωy Qy Q Вþ 20 В Query Match
Best Local Similarity
Matches 1231; Conserv 2960 2720 3200 3140 3080 3020 2900 2840 2780 187 127 487 427 367 307 247 607 547 67 7 aatctgaagcttaataagtatgaactaaaatgcatgtaggtgtaagagctcatggagagc atggaatattgtatccgaccatgtaacagtataataactgagctccatctcacttcttct atggaatattgtatccgaccatgtaacagtataataactgagctccatctcacttcttct aatgcaagcttaaataagtatgaactaaaatgcatgtaggtgtaagagctcatggagagc aaatagtacaaaaacaaatgtgtactataagactttctaaacaattctaactttagcatt aaatagtacaaaaacaaatgtgtactataagactttctaaacaattctaactttagcatt gtgaacgagacataagtgttaagaagacataacaattataatggaagaagtttgtctcca gtgaacgagacataagtgttaagaagacataacaattataatggaagaagtttgtctcca 31.0%; nilarity 99.4%; Conservative 0; Score 1226.8; DB 2 Pred. No. 1.4e-164; 0; Mismatches 7; 20; Indels Length 1244; 0; Gaps 426 3079 3019 2899 126 2779 3199 2959 186 66 666 486 366 246 606 0,

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RESULT
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ID AASO
XX AASO
XX 14-M
AX BOV1
XX Chym
KW Pre-
KW barl
KW Squa
XX Squa
XX Squa
XX Squa
XX Ghym
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                                                                                                                                                                                                                                                                                                                                       pre-pro-chymosin; rape seed; sunflower; cotton; barley; oats; sorghum; Arabidopsis thaliana; pot safflower; oll palm; ground nut; Brazil nut; coo
                                                                                                                                                                     sig_peptide
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 WO200114571-A1
                                                                         mat_peptide
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                                                                                                                                                                                                                                                                                                                             jojoba;
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                                                                                                                                                                                                                                                                                                                                                                                                transcription regulator; terminator sequence; soybean,
                                                 /note= "Pro
202..1170
/*tag= d
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                                                                                                                                                                                                                                                                                                                                         on; tobacco; alfalfa; w)
potato; flax; linseed;
coconut; castor; coriar
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                                                                                                                                                                                                                                                                                                                                                                              wheat;
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Best Local Similarity
Matches 1173; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents a DNA which encodes a bovine chymosin polypeptide. Chymosin can be produced in a plant seed through introduction of a chimeric nucleic acid molecule, comprising a nucleic acid sequence encoding a chymosin polypeptide operatively linked to transcription regulator and terminator sequences, into a plant cell. The sequences are useful for producing plant seeds, in particular seeds of soybean, rape seed, sunflower, cotton, corn, tobacco, alfalfa, wheat, barley, oats, sorghum, Arabidopsis thaliana, potato, flax/linseed, safflower, oil palm, groundnut, Brazil nut, coconut, castor, coriander, squash, jojoba and rice.
                                                                  1974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing chymosin in seeds of plants such as rice, flax, rape
transforming plant cell with a nucleic acid encoding chymosin
linked to transcription regulator and terminator sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing
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gatactggttcctctgacttctgggttccctctatctactgcaagagcaatgcctgcaag
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                                                                                                                                  gatactggttcctctgacttctgggttccctctatctactgcaagagcaatgcctgcaag
                                                                                                                                                                            agtcaatactttgggaagatctacctcggaaccccgcctcaagagttcaccgttctcttt
                                                                                                                                                                                                                       agcagcaagtactccggcttcggtgaagttgctagcgtgccacttaccaactaccttgat
                                                                                                                                                                                                                                                                                                             gctgttactcacgctgctgagatcacccgcattcctctctacaaaggtaagtctctccgt
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 1173; DB 22;
Pred. No. 5.3e-157;
0; Mismatches 0;
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RESULT
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XX CAD1
DF CAD1
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KW Soyk
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                                                                                                                                                                                                                                                                                                                         an; allergen; transgenic plant; P34 protein; Gly m Bd 30K; Gly m 1; an vacuolar protein; Gly m IA; Gly m IB; rGLY m3; Glycinin Gl; b; food; infant formula; animal feed; coating; salad oll; syrup; ing oil; roasting oll; frying oil; cracker; confectionery product; food; topping; sauce; batter; breading mixture; baking mix; dough;
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cc expression constructs to lower soybean vacuolar protein, commonly known cc as p34 (Gly m Bd 30K or Gly m 1) and other allergens such as Gly m IA, CC Gly m IB, rGLY m3 or Glycinin G1 (alaBlb). The allergen content of the expression is reduced by sense suppression which is accomplished by using ct the expression construct that comprises a nucleic acid fragment encoding ct transgenic soybean plants which can be used to make hypoallergenic cc soybean products which can be used to make hypoallergenic cc soybean products which can be used in a variety of food (e.g. infant cc formulas) and animal feed applications. The oil made from seeds of the hypoallergenic transgenic soybean plants can be used as ingredients, as coatings, as salad oils, as spraying oils, as roasting oils, and snack foods, confectionery products, syrups and toppings, sauces, batter and breading mixtures, baking mixes and doughs. The present cc sequence is a DNA encoding kunitz soybean trypsin inhibitor (KSTI cc KTi3), a minor soybean seed allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant expression construct to lower allergen (e.g. Gly content of a soybean, comprises a nucleic acid fragment encot allergen, useful for producing soybean plants which can be us soybean products
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                                                                                                                                                                                                                                                                                                        tggatagtcagtactttgggaagatctacctcgggaccccgccccaggagttcaccgtgc
                                                                                                                                                                                                                                                                                                                                                                                               gcatcagcagcaagtactccggcttcggggaggtggccagcgtgcccctgaccaactacc
                                  tgttctcggtttacatggacaggaatggccaggagagcatgctcacgctgggggccatcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               having region in the food prodn. eg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 898.8;
Pred. No. 2.3e
0; Mismatches
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) large amts of the protein by

1 overcome the shortage of

comachs and increasing cheese

win. of yoghurt, butter and
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.3e-118;
es 137;
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The DNA is that of a mammalian gene (open reading frame) encoding chymosin. The gene was placed in operable linkage with the al-3 promoter (see AAT03005). The al-3 gene controls the production of geranyl geranyl pyrophosphatase (GGPP) synthetase. GGPP is a precurso for carotenoids and xanthophylls. It has been shown that exposure to light increases the transcription level of GGPP synthetase 15-45 fold. Light activates a number of genes in the common bread mould, Neurospor This can be used to regulate the expression of genes encoding
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for light induced expression in filamentous
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xpression; control; chymosin;
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                                                                                                          2329
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                                                                                   agttcactgtggacagtgtcaccatcagcggtgtggttgttgtggcctgtgagggtggctgtc
                                                                                               aattcactgtggacagtgtcaccatcagcggtgtggttgttgttgcatgtgaaggtggatgtc
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         ttcagcaagctattggagccacacagaaccagtacggtgagtttgacatagattgcgaca
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87.4%;
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Pred. No. 3.6e
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No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 16;
.6e-118;
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Best Local Similarity
Matches 763; Conser
                                                                                                         Also claimed is E.coli JM83/pLC7 (ATCC 39325) which is transformed with pLC7 contg. the prorennin derived sequence fused in phase with B-galactosidase. The pLC7 prorennin expression plasmid includes sequences which code for both the pseudorennin and mature rennin cleavage sites between AAs 28-29 and AAs 42-43, respectively.
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                   999ccaaccacctcgttgggctagctaaagcaatctga
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Best Local Similarity
Matches 980; Conserv
                                                                                                                                                                                                                                       The inventors claim a DNA segment contg. GAL1 promoter linked to gene - useful for direction of expression of the gene in yeast ce The recombinant material carrying a GAL1 promoter of the yeast ce galactokinase gene may be used in expressing a desired protein, e bovine growth hormone, interferon, prorennin or preprorennin, in yeast cell. Strains of Saccharomyces cerevisiae producing the polypeptides are produced. Yeast strains deposited as ATCC 20643, 20661, 20662 and 20663, strain designations CGY 196, 457, 461 and 528, resp. are new.
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DB; AAP40218.
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                                                  gcatcagcagcaagtactccggcttcggtgaagttgctagcgtgccacttaccaactacc
                                                                                          tccgtaaggcgctgaaggaacatggacttctagaagacttcttgcagaaacaacagtatg
                                                                                                                        tettegeteteteceagggegetgagateaceaggatecetetgtacaaaggcaagtete
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                                      gcatcagcagcaagtactccggcttcggggaggtggccagcgtgcccctgaccaactacc
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Pred. No. 3.8e-118;
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Prorennin; alpha-S1-casein mammary gland; ss.

gene; insulin-like growth factor

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Rennin 06-JAN-1992

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/note= "CDS
850..1202
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1203..1442
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                                                                                                                                                                                                                                                                                                                                                                                                                                   fragment of psbsorprnr (oleosin-chymosin
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1443..2733
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22-FEB-1991;
16-NOV-1993;
30-DEC-1994;
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The DNA which encodes a chimeric fusion protein that consists of the oil-body targeting sequence, a transcription regulation sequence an DNA of the protein of interest can be used to produce antibodies, glycanases, hormones, proteases, protease inhibitors, seed storage proteins, thrombin inhibitors, hirudin, interleukins, chymosin, cys xylanase, carp growth hormone, zein or a collagenase.

The enzyme may be cleaved from the oil body protein or used in
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                                                                                                                                                                                                                                                                                                                                           association with the oil body fraction.

Allows production of commercially important proteins on a superior to production by conventional systems. The expressed heterologous protein can be easily separated from host cell components due to the use of the oil body as a carrier protein.
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                                            gacttctgggttccctctatctactgcaagagcaatgcctgcaagaaccaccaaagattc
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Hidaka M;
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                ctgtctccaacattgtggacattcaacagacagtaggacttagcacccaagaaccaggtg
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DB; AAP40078.
                                                    ccttgtctatacactacggtacaggtagcatgcaaggaatcttaggctatgataccgtca
                                                                                      gcaagaaccaccaaagattcgatccgagaaagtcgtccaccttccagaacttaggcaaac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e removed and are not essential to use of the
ssidon. The gene may be ligated into plasmid
ssed in E. coli. The resulting expressed en
milk-clotting enzyme used in cheese-making.
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                                                                                                Disclosure;
                                                                                                                                           Kluyveromyces host cells for producing used for highly efficient prodn. of eg plasminogen activator or human serum al
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A1892188 mj84c05.y
BG937697 1Abo05E01
A11266975 mj81e03.x
BG937723 1Abo05D06
AK004109 Mus muscu
BG938086 1Abo11A08
AA028632 mi14c08.r
A1479358 tm27e07.x
A1324867 mi82b01.x
A1385490 mj81e03.y
AK008959 Mus muscu
AW868692 MR1-SN006
        AK008886 Mus muscu
AI322423 mi82b01.y
AW868716 MR1-SN006
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ALIGNMENTS

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                                                                                                              source
                                                                                                                                                                                                                                                                                                               Unpublished (2001)

Contact: Dr. Stephen Moore

Beef Genomics Laboratory

Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Ec
Tel: 780 492 0169

Fax: 780 492 4265
                                                                                                                                                                                                                                                Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVCHYMOA (bovine chymosin a
mrna) in main database at high score of 928.0 and E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae; Bos.
1 (bases 1 to 472)
Moore, S.S., Hansen, C., Li, C.
cDNA's from bovine abomasum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
BG938320
BG938320.1 GI:14337692
EST.
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/clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
/tissue_type="@astrointestinal tissue (GIT)"
/cell_type="Epithelial"
                                                                        /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                   AI892188 631 bp mRNA linear EST 15 mj84c05.yl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:482792 5' similar to TR:Q28950 Q28950 PREPROCHYMOSIN
                                                                                                                        Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Pe,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ri,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                           Unpublished (1999)
Contact: Marra M/MashU-NCI Mouse EST Project
Washington University School of Medicine
Washington University School of St. Louis
                                                                                                                                                                                                                        Mammalia; Eutheria;
1 (bases 1 to 631)
                                                                                                                                                                                                                                                                                                                                     PRECURSOR ;, mRNA sequence. AI892188
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clone is
              mouseest@watson.wustl.edu
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a 143 c 131 g 94 t
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/lab_host="XL1-BlueMRF'-strain"
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                                                                                           CACTGTCACAGTCTCTGATATTGTAGTGTCCCATCAGACTGTGGGCCTGAGTACCCAGGA
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gtactggcaattcactgtggacagtgtcaccatcagcggtgtggtggttgttgcatgtgaagg
                                                     agctattgatccatcctactacacaggatctcttcactgggttccagtcactgtgcagca
                                                                                                                                                  TTTTGCCTCCAAATACTCAGTACCCATATTTGACAACATGATGAACAGGCACCTGGTGGC
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                                        460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Possible reversed clone: similarity MGI:293536
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Location/Qualifiers
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73.0%;
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Pred. No. 6.5e-37;
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                                            ACTACACAGGGTCCCTGCACTGGGTGCCCGTGACAGTGCAGCAGTACTGGCAGTTCACTG
                                                                                                     TTTACATGGACAGGAATGGCCAGGAGAGCATGCTCACGCTGGGGGCCATCGACCCGTCCT
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BG937697.1
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CDNA's from bovine abomasum tissue
Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cow.
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dept of AFNS, University of Alberta 410 Agri/For, Dept of AFNS, U of A, Tel: 780 492 0169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVCHYN
mrna)in main database at high score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: T3 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 780 492 4265
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                                            /note="Organ: Abomasum; Vector:
I; Site_2: Xho T"
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="Bovine Abomasum cDNA Library"
/clone_Tib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GI'
/cell_type="Epithelial"
                                                                                                                                                                                                                                                                                                                                                         /dev_stage="Young adult"
/lab_host="XL1-BlueMRF'-strain"
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130 c 119 g
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AI326975.1
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., D

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore,

Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
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314 286 1810
double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Patima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."
                                                                                                                              /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:482524"
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Local Similarity 71.4%;
hes 474; Conservative
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                                                                             sequence.
BG937723
BG937723.1
EST.
                                                                                                                      BG937723
1Abo05D06
                            Bos taurus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Cetartiod
Bovidae; Bovinae; Bos.
 Moore, S.S., cDNA's from
                                                                     COW
                  (bases 1 to 399)
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Hansen, C., Li, C. bovine abomasum
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                                      Chordata; Craniata; Vertebra:
Cetartiodactyla; Ruminantia;
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Pred. No. 2.9e-34;
0; Mismatches 183;
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          Meng, Y.
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                                                 Euteleostomi;
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                                                                                                                                            CCTATACCAGCCAAGACCAGGGCTTCTGTACCAGTGGCT
                                                                                                                                                                                                                          GCTACATGCCCACTGTGGTCTTTGAAATCAATGGCAAAATGTACCCACTGACCCCCTCCG
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Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
AK004109 1347 bp mRNA linear HTC 19-JAN Mus musculus 18 days embryo whole body cDNA, RIKEN full-length enriched library, clone:1110035E17:PEPSINOGEN F, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence best matches q mRNA, complete cds)in main E-value of 0.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: smoore@afns.ualberta.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: T3 primer
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/tissue_type="Gastrointestinal tissue (Gcell_type="Spithelial"
/dev_stage="Young adult"
/dev_stage="Young adult"
/lab_host="XII-BlueMRF'.strain"
/note="Organ: Abomasum; Vector: Uni-2ZAF
I; Site_2: Xho I"
I; Site_2: Xho I"
I Site_77 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Bovine Abomasum cDNA Library"
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/db_xref="taxon:9913"
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Pred. No. 1.9e-32;
0; Mismatches 47
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E 5 (bases 1 to 1347)

KS (bases 1 to 1347)

KS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Adachi, J., Aizawa, K., Akahira, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Hume, D., Imotani, K., Ishii, Y., Konno, H., Kouda, M., Koya, S., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Mishi, K., Nomura, K., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Saito, H., Saito, H., Sakai, Y., Shibata, Y., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                          Please visit our web site (http://genome.gsc.riken.go.jp/) further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Functional annotation of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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Sciurognathi;
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Best Local Similarity
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caggagagcatgctcacgcttggagctattgatccatcctactacacaggatctcttcac 2297
                                          TGGCTACAAGGCCTCATCCCCCAGAATCTCTTTGCCTTCTACTTGAGCAGCAAGGATGAA
                                                                                 atgaaccgacacctagtagctcaagacttgttctcggtttacatggacag---gaatggc 2237
                                                                                                                                                       cttggtatggcatacccatcgctcgcgtcagagtactcgatacctgtgtttgacaacatg
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                                                                                                                                                                                                                                                                                                                                   caaggaatcttaggctatgataccgtcactgtctccaacattgtggacattcaacagaca 2060
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FGLSSLEEPGIFMEYAVFDGILGIGYPNLGLQGITPVFDLMLAGGLIPQNLFAFYLSSK
DEKGSMLMLGGYDPSYYHGELHWYDVSKPSYMGLAVDSISMNOEVIACDGGCQGIMDT
GTSLLTGPRSSIVNIONLIGAKASGDGEYFLKCDTINTLPDIYFTIGSYTYPVPASAY
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/codon_st
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1332. .1337
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/dev_stage="18 days embryo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="C57BL/6J"
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58.2%;
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Pred. No. 8.7e-30;
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BG938086
BG938086.1
EST.
                                                                                                          FORWARD: M13 Forward
BACKWARD: M13 Reverse
Seq primer: T3 primer
High quality sequence
                                                                                                                                                                                                                    mRNA, complete cds) in E-value of 0.0
                                                                                                                                                                                                                                    Email: smoore@afns.ualberta.ca
Email: smoore@afns.ualberta.ca
The sequence best matches gb:BPU19786 (Bos primigenius
The sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the seque
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410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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cDNA's from bovine abomasum
Unpublished (2001)
Contact: Dr. Stephen Moore
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/organism="Bos taurus"
/db_xref="taxon:9913"
                                                              Location/Qualifiers
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                                              Tel:
                                                              WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                               EST
                                                                                                                                   Contact: Marra M/Mouse EST Project
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      mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                             479 bp mRNA linear mil4c08.rl Soares mouse p3NMF19.5 Mus musculus cDNA IMAGE:463502 5' similar to SW:CHYM_BOVIN p00794 PROC PRECURSORS ;, mRNA sequence.
                                 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque, Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
The WashU-HHMI Mouse
                   Waterston, R.
                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                 Mus musculus
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I; Site_2: Xho I"
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/sex="Two males and one female mixed"
/tissue_type="dastrointestinal tissue (GIT)"
/cell_type="Epithelial"
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/lab_host="XL1-BlueMRF'-strain"
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1 to 479)
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                       AI479358 505 bp mRNA linear EST 14-tm27e07.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157828 3' similar to TR:Q28950 Q28950 PREPROCHYMOSIN
AI479358
           PRECURSOR ;,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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/db_xref="taxon:10090"
/clone="IMAGE:463502"
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                                                                                                                                                                                                                                                                                                                                                                   agctacatgcctacagttgtctttgagatcaacggcaagatgtacccactgaccccctcc
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                                                                                                                                        cagaaatggatcttggggagatgtgttcattcgtgagtactacagcgtctttgacagggcc
                                                                                                                                                                                                                                                         gcctataccagccaggatcaagggttctgcaccagtggattccagagtgagaaccattcc
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AATAACCGTGTGGGGGCTGGCGAAGGCTGTCTGA 113
                                                                                                                                                                                                                           GCCTATACCAGCCAGGACCAGGGCTTTTGCACCAGTGGTTTCCAGGGTGACTATAGTTCC
                                                                                                                                                                                                                                                                                                                                         AGCAGCATTCCCACGGCTGTTTTTGAGATCCACGGCAAGAAGTACCCCCTGCCACCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGGCCATTGGAGCCACTGCGGGCCAGTACAATGAGTTTGACATCGACTGCGGGCGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCCTGGACACCGGCACCTCCCTGCTGGTGGGGGCCTGGCGGCAACATCCTCAACATCCAG
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NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 608 Std Error: 0.00 Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
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1 (bases 1 to 505)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DHIOB"

//lab_host="DHIOB"

//note="Organ: pooled: Vector: pT7T3D-Pac (Pharmacia) with /note="Organ: pooled: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares_NFL_T_GBC_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:2157828"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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77.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 249.6; DB y;
Pred. No. 5.5e-23;
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RESULT 10
AI324867/c
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                                                                                                                                                                                                               Matches
                  2363 ggttgttgcatgtgaaggttggatgtcaagctatcttggataccggtacgtccaagctggt 2422
                                                                                      2303 tccagtcactgtgcagcagtactggcaattcactgtggacagtgtcaccatcagcggtgt 2362
                                                                                                                                                            2243 gagcatgctcacgcttggagctattgatccatcctactacacaggatctctttcactgggt 2302
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                                                                    486
                                                                                                                                           546
                                                                                                                                                                                                                                Local Similarity
                                                                    GAGCATGCTCACACTGGGGGGCCATCGATCAGTCATACTTCATAGGCTCACTGCACTGGGT 487
AGTGGTGGCTTGTCAAGGTGGCTGCCCTGCCGTTCTGGACACAGGCAATGCCCTGTTGAC
                                                                                                                                                                                                                 343;
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mi82b01.x1 Soares mouse
rmage:473065 3' similar
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This clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 546)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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AI324867.1 GI:4059296
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Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                      134
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314 286 1810
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:473065"
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                                                                                                                                                                                                                              6.2%;
                                                                                                                                                                                                              Score 246; DB 9;
Pred. No. 1.5e-22;
0; Mismatches 135
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                                                                                                                                                                                                              Mismatches 135;
                                                                                                                                                                                                                                             Length 546;
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCCAGTGGCTTC----AAGCAGGGCTCCCACATGTGGATCCTTGGGGATGTTTCAT
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Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI385490 517 bp mRNA linear EST 27-JAN-1999 mj81e03.y1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE: 82524 5' similar to TR:Q28950 Q28950 PREPROCHYMOSIN
                                                                                                                                                                                                         High
                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further;
                                                                                                                                                                                                                                                                                                                                                                                                               Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/WashU-NCI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                This read is a RESEQUENCE of a previously This read has been verified (found to hit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                           Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                            Possible reversed
                                                                                                                                                                                                                                                               correct orientation)
                                                                                                                                                                                                                                                                                                                   MGI:293268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nouse mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases
                                                                                                                                                                                    quality sequence stop: 442
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            314 286 1800
314 286 1810
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st str
was primed with a Not I - oligo(dT) primer [5'
                                                                                            /clone_lib="Soares mouse p3NMF19.5"
                                                                                                           /db_xref="taxon:10090"
/clone="IMAGE:482524"
                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria;
1 to 517)
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   1st strand cDNA [5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gatctacctcggaaccccgcctcaagagttcaccgttctcttttgatactggttcctcttga 1870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATCGGGGTGGTGGCCAGTGAGCCTCTGATCAACTATCTAGATAGTGAGTACTTTGGAAC
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                                                                            Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                               Mus musculus (strain:C57BL/6J) adult male stomach cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
                   Carninci, P.,
                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                            AKO08959 1385 bp mRNA linear HTC 19-JAN-2002 Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210416016:homolog to GASTRICSIN PRECURSOR (EC 3.4.23.3) (PEPSINOGEN C), full insert sequence.
                                                                                                                                                                                       clone:2210416016.
                                                                                                                                                                                                                                 HTC; CAP trapper.
                                                                                                                                                                                                                                                    AK008959.1 GI:12843460
   Itoh, M., Konno, H.,
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                                   (sites)
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70.9%;
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], CDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 5.0 and subtraction Rot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., Sikikawa,T., Ozawa,K., Sayashizaki,Y., Sikikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., Sikikawa,T., Ozawa,K., Sayashizaki,Y., Sikikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., Sikikawa,T., Ozawa,K., Sayashizaki,Y., Sikikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., Muramatsu,M., Inoue,Y., Kira,A., Muramatsu,M., Muramatsu,M., Inoue,Y., Kira,A., Muramatsu,M., Mu
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Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute (Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute (Institute (Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pequence [7] and satt. Cloning sites, 5' end: XhoI; 3' end: SstI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             = 25.0. Second secuence [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for feature visit our web site (http://genome.gsc.riken.go.jp/)
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Hayashizaki,Y.
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/tissue_type="stomach"
/clone_lib="RIKEN full-length
/dev_stage="adult"
                                                                                                                                                                                                                                                                            /strain="C57BL/6J"
/db_xref="MGD:MGI:1895643"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                   /clone="2210416016"
                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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                                                                                      ACCACCGCCTTGCAGGGCATGTTGGGGGGAGGGCGCTCTGTCCCAGCCCCTCTTCGGTGTC
                                                                                                                                                                                                                                                                                cactacggtacaggtagcatgcaaggaatcttaggctatgataccgtcactgtctccaac
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tcctactacacaggatctcttcactgggttccagtcactgtgcagcagtactggcaattc
                              TACCTTGGCAGCCAGCAGGGTCTAACGGCGGGCAGATTGTGTTCGGTGGCGTGGACGAG
                                                        tacatggacaggaatggccaggagagcat----gctcacgcttggagctattgatcca
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/protein_id="Bab25990.1"
/db_xref="GI:12843461"
/translation="mkmmyvallclplleaalirvplkkmksiretmkeogvikdfik
/translation="mkmmyvallclplleaalirvplkkmksiretmkeogvikdfik
vhkydpogkylhegkfeoysulyepmaymdasyygeisjigfpeogrifulpdgssnlwy
ssyycoseactthtrynpsksstyytogotfsloygfigsitgfffoydtlrvosiovpn
oeffglseneftnfyxaofdoimglaypglsscgattalogmlgealsoplegvylo
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GIVDTGTSLLVMPAQYLNELLQTIGAQEGEYGQYFVSCDSVSSLPTLTFVLNGVQFPL
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CTGAACGCTGAGAGTGGCCAGCCCCTCTGGATCCTCGGGGGATGTCTTCCTCAGGTCTTAC
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl~&t2=MR1-SN0064-150
500-004-a03&t3=2000-05-15&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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MR1-SN0064-150500-004-a03
                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
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1 (bases 1 to 619)
                                                                                                                                               Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                            Fax: +55-11-2707001
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                                                                     quality sequence start: 10 quality sequence stop: 619 Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Eutheria; Primates;
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ta Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                      1388 bp mRNA linear HTC 19-JAN-2002 Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:22104101.06:homolog to GASTRICSIN PRECURSOR (EC 3.4.23.3) (PEPSINOGEN C), full insert sequence.

KK008886
                                                  Mus musculus
                             Eukaryota; Metazoa;
                                                                                      clone: 2210410L06.
                                                                                                                 Mus musculus (strain:C57BL/6J) adult clone_lib:RIKEN full-length enriched
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                                                                                                                                                                    CAP trapper.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue mRNA and cDNA amplification were performed under low stringency conditions." 201 c 147~{\rm g} 145~{\rm t}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="Adult"
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  Eutheria;
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Pred. No. 2.8e-21;
0; Mismatches 215
Craniata; Vertebrata;
Sciurognathi; Muridae;
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                                                                                                              male stomach cDNA mouse cDNA library
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  Muridae; Murinae; Mus
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                             Euteleostomi;
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  source
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E 5 (bases 1 to 1388)

RS Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, I., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and
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                                                                                                                                                              further details.

further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5 GAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3 ], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction Rot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission

Direct Submission

Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (REKN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes genome Res. 10 (10), 1617-1630 (2000)
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                                                                                URL:http://genome.gsc.riken.go.jp/,
Fax:81-45-503-9216)
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Hayashizaki,Y.
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                                                                                                                                         sequence
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                       ACCCGCTACAACCCCAGCAAGTCCTCCACCTACTACACTCAAGGGCAGACCTTCTCCCTG
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TACGCCCAATTTGACGGGATCATGGGCCTGGCCTACCCCGGCCTGTCTTCAGGGGGGCGCC
                                                                                        ATCCAGGTCCCTAACCAGGAGTTCGGCCTGAGTGAGAATGAGCCTGGCACCAATTTTGTC
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NHKYDPGQKYHFGKFGDYSVLYEPMAYMDASYYGEISIGTPPQNFLYLEDTGSSNLWV
SYYYCQSEACTHTRYNPSKSSTYYTGGQTFSLQYGTGSLTGFEGYDTLRVQSIQVPN
QEFGLSENEBGTNFYYAQFDGIMGLAYPGLSSGGATTALQGMLGEGALSQPLFGVYLG
SQQGSNGGQIYFGGVDENLYTGELTWIPVTDELYWQITIDDFLIGNQASGWCSSSGCQ
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/clone_lib="RIKEN full-length enriched
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/strain="C57BL/6J"
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                      Marra, M., Hillier, L., Allen, M., Bowles, M., Dittrich, N., Dub
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                        correct orientation)
Putative full length read
                                                                                                                                This read is a RESEQUENCE of
This read has been verified
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                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
Contact: Marra M/Mouse EST Project
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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Sequence 6, Appli
Sequence 15, Appl
Patent No. 5210327
Patent No. 5200327
Patent No. 5200327
Sequence 6, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 16, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 11, Appli
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ALIGNMENTS	US-08-998-416-288	US-08-213-419B-3	US-08-487-826B-13	US-08-947-823-1	US-09-150-741-1	US-08-446-855A-1	US-08-998-416-186	5231168-1	US-08-544-332-32	US-08-107-755A-32	US-07-991-867B-32	US-09-316-083-2	US-08-544-332-8	US-08-107-755A-8	US-07-991-867B-8	US-08-852-629-15	US-08-852-629-11	US-08-487-826B-13	
	Sequence 288, App	Sequence 3, Appli	Sequence 13, Appl	Sequence 1, Appli	Sequence 1, Appli		Sequence 186, App	Patent No. 5231168	Sequence 32, Appl	Sequence 32, Appl	32,	Sequence 2, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 15, Appl	Sequence 11, Appl	Sequence 13, Appl	

US-08-240-372-2

Sequence 2, Application US/08240372 Patent No. 5741665

GENERAL INFORMATION:

APPLICANT: KATO, ELIE K.
APPLICANT: STUART, W. DORSEY
TITLE OF INVENTION: LIGHT-REGULATED PROMOTERS FOR PRODUCTION
TITLE OF INVENTION: OF HETEROLOGOUS PROTEINS IN FILAMENTOUS FUNGI
NUMBER OF SEQUENCES: 2

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; TYPE: nucleic acid
; STRANDEDNESS: singl
; TOPOLOGY: linear
US-08-240-372-2
Query Match
Best Local S
Matches 982
                                                                                                                                                                                                                                                                                                                                                                        STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION UDATA:
APPLICATION NUMBER: US/08/240,372
FILING DATE: 10-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                  TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 3918
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
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Similarity 87.4%;
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Score 897.4; DB 1;
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Matches 972;
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Patent No. 5948682
GENERAL INFORMATION:
APPLICANT: Moloney, Maurice M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 2733 base pairs
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,021A
FILING DATE: April 25, 1997
CLASSIFICATION: 800
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LOCATION:
FEATURE:
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NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 93
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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ADDRESSEE: BERESKIN & PARR
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CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
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M5H 3Y2
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Preparation of Heterologous
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; APPLICANT: BRAKE, ANT
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                               NUMBER OF SEQUENCES: 23
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 09-APR-1990
PRIOR APPLICATION DATA:
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N: DNA CONSTRUCTS CONTAINING A KLUYVEROMYCES
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                                                                                                                                                                                         TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07/
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING NUMBER: US 07/
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,76
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TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 832 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
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APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 435
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                                                                  MOLECULE TYPE:
DESCRIPTION:
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CITY: Alexandria
STATE: Virginia
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                                                                                                    TOPOLOGY: linear
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                                                                  Other nucleic
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OF BIOACTIVE HUMAN GRANULCCYTE MACROPHAGE COLONY
STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
PROTEINS FROM STREPTOMYCES
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APPLICANT: GARVIN, ROBERT T.;MALEK, LAWRENCE T.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETION
;BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY STIMULATING
;FACTOR (CM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM
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                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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          caagaaccaccaaagattcgatccgagaaag 1940
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Pred. No. 3.9e-33;
0; Mismatches 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; APPLICANT: GARVIN, ROBERT T.; MALEK, LAWRENCE T. TITLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETIC; BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY STIMULATING; FACTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   APPLICANT: GARVIN, ROBERT T.
APPLICANT: MALEK, LAWYENCE T.
TITLE OF INVENTION: AN EXPREST
TITLE OF INVENTION: OF BIOACTITITLE OF INVENTION: STIMULATING
TITLE OF INVENTION: PROTEINS F.
                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTUBARE: Patentin Release #1.0,
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                     CURRENT APPLICATION DATA:
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CITY: Alexandria
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                                                                                                                                 COUNTRY: USA
ZIP: 22313-0299
 APPLICATION NUMBER:
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OF BIOACTIVE HUMAN GRANULCYTE MACROPHAGE COLONY
STIMULATING FACTOR (GM.CSF) AND OTHER HETEROLOGOUS
PROTEINS FROM STREPTOMYCES
US/08/318,193
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Pred. No. 1.8e-32;
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                                                                                                                                                         Sequence 6, Application Patent No. 6232454
GENERAL INFORMATION:
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Best Local Similarity
Matches 245; Conserv
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                                           APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl
APPLICANT: Baugh, Mariah
TITLE OF INVENTION: HUMAN PROTEINASE MOLECULES
NUMBER OF SEQUENCES: 9
                            CORRESPONDENCE ADDRESS
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
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CLASSIFICATION:
ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DESCRIPTION: Synthetic DNA oligonucleotide
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76.3%;
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Pred. No. 2.1e-32;
0; Mismatches 76;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
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                   2114
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                                                                                                                                                     1994 tagcatgcaaggaatcttaggctatgataccgtcactgtctccaacattgtggacattca 2053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 CTCTGAGTTCTGGAAATCCCATAATTTGGACATGATCCAGTTCACCGAGTCCTGCTCAAT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 CAGGGTGCCCCTCAGGAGGCATCCGTCCCTCAAGAAGAAGCTGCGGGCACGGAGCCAGCT 163
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: PANCT
CLONE: 1515165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650-845-4166
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                                                                                                                                                                                                              gagaaagtogtocacottocagaacttaggcaaacoottgtotatacactacggtacagg 1993
                                                                                                                                                                                                                                                                                                                                              ctacctcggaaccccgcctcaagagttcaccgttctctttgatactggttcctctgactt 1873
                                                                                acagacagtaggacttagcacccaagaaccaggtgatgtcttcacctatgcagaattcga
tggcatccttggtatggcatacccatcgctcgcgtcagagtactcggatacctgtgttttga
                                                     CCAGCAGTTTGGAGAAAGTGTCACAGAGCCAGGCCAGACCTTTGTGGATGCAGAGTTTGA
                                                                                                                          GAGCTTGTCCGGGATCATTGGAGCCGACCAAGTCTCTGTGGAAGGACTAACCGTGGTTGG
                                                                                                                                                                                          TTCCCAGTCCAGCACATACAGCCAGCCAGGTCAATCTTTCTCCATTCAGTATGGAACCGG
                                                                                                                                                                                                                                                            CTGGGTCCCCTCTGTGTACTGCACTAGCCCAGCCTGCAAGACGCACAGCAGGTTCCAGCC
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Pred. No. 8.3e-31;
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US-08-723-938-4
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                                                                ; CLONE: US-08-723-938-4
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Best Local Similarity
Matches 421; Conser
           Query Match
Best Local
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                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                    FRAGMENT TYPE:
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         644 CAACATGATGGCTCAGAACCTGGTGGACTTGCCGATGTTTTCTGTCTACATGAGCAGTAA 703
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                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                            ANTI-SENSE:
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                                                                  MMEUIA: LUAL LIBRARY: LUAL 312099
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CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP:
                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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TWO NOVEL HUMAN CATHESPIN PROTEINS
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            3.7%;
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 Score 146.6; D
Pred. No. 1.7e-
0; Mismatches
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 DB 1;
e-21;
399;
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US-09-080-538-4
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                                                                                                                                                                   APPLICANT: Coleman, Roger TITLE OF INVENTION: TWO NOVEL
COMPUTER READABLE FORM:
                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                        APPLICANT: Bandman, APPLICANT: Coleman,
                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                               997
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                   COUNTRY: UZIP: 94304
                                                                    STREET: 3174 PO:
CITY: Palo Alto
                                                         STATE:
                                                                                          ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
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Best Local S
Matches 421
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SEQUENCE CHARACTERISTICS:
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LIBRARY: LUNGN
CLONE: 312099
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
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nes 421; Conserv
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REGISTRATION NUMBER:
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COMPUTER: IB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                              GGAGCAGGGGCTATTGGATAAGCCTGTCTTCTCCTTTTACCTCAACAGGGACCCTGAAGA
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                                                                               gaaccgacacctagtagctcaagacttgttctcggtttacatggacaggaatggccagga 2242
                                                                                                                                                                  tggtatggcatacccatcgctcgcgtcagagtactcgatacctgtgtttgacaacatgat 2182
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Pred. No. 1.7e-21;
0; Mismatches 399;
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US-08-974-691-7
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                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,126
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF 166
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                           TELEFAX: 404-873-8795 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2294
                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 20-NOV-1997
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                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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APPLICANT: Tang, Jordan
TITLE OF INVENTION: Cloning
MOLECULE TYPE:
HYPOTHETICAL:
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STREET: St.
CITY: Atlan
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polonia
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60 FILING DATE: 20-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Atlanta
STATE: GA
                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 30309-3450
                                             STRANDEDNESS: single
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                                                                           LENGTH:
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US-09-008-271A-16

Sequence 16, Application Patent No. 6203979
GENERAL INFORMATION:

6, Application 6203979

US/09008271A

APPLICANT:

Bandman, Hillman,

Olga Jennifer

RESULT

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; ORIGINAL SOURCE:
; ORGANISM: HOM
US-08-974-691-7
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                         CTTGCTGGCTGGGGAGTACATCATCCTGTGCTCGGAAATCCCAAAGCTCCCCGCAGTCTC
                                                                      gaaccagtacggtgagtttgacatagattgcgacaaccttagctacatgcctacagttgt
                                                                                                                                                             GGGCCCAGGGCTGACTCTCTGTGCCAAGGGCTGTGCTGCCATCCTGGATACGGGCACGTC
                                                                                                                                                                                                                                                                                      g-----agcatgctcacgcttggagctattgatccatcctactacacaggatctct
                                                                                                                                                                                                                                                                                                                                                                             TGGAATCCTGAGCGAGGACAAGCTGACTATTGGTGGAATCAAGGGTGCATCAGTGATTTT
CTTCCTTCGGGGGGGTCTGGTTTAACCTCACGGCCCATGATTACGTCATCCAG
                                                                                                                        caagctggtcggacctagcagcgacattctcaacattcagcaagctattggagccacaca
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                                                                                                         Similarity 50.,
21; Conservative
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Pred. No. 1.9e-21;
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US-09-008-271A-16
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Best Local
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SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
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FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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CGGGGAGGCTCTCTGGGAGCCCAGCCTGGTCTTCGCCTTTTTGCCCCATTTTTGATGGGATATT
                 aggacttagcacccaagaaccaggtgatgtcttcacctatgcagaattcgatggcatcct 2122
                                                                                                                            TAGCTCCTTCCAGGCCAATGGGACCAAGTTTGCCATTCAATATGGAACTGGGCGGTAGA
                                                                                                                                                 gtccaccttccagaacttaggcaaacccttgtctatacactacggtacaggtagcatgca
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                                                                                              GAGATGCCACTTCTTCAGTGTGCCCTGCTGGTTACACCACCGATTTGATCCCAAAGCCTC
                                                                TGGAATCCTGAGCGAGGACAAGCTGACTATTGGTGGAATCAAGGGTGCATCAGTGATTTT
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CLONE: 8
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FILING DATE: 16-Jan-1998
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
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REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458
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                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Shah, Purvi
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Corley, Neil C.
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Pred. No. 1.
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APPLICANT: KINCHL, A
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08631097 Patent No. 5968816
                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                   STREET: YOU CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1391
                                                                                                                                                             APPLICATION NUMBER: PCT/US94/11598 FILING DATE: 12-Oct-94 ATTORNEY/AGENT INFORMATION:
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                                                                                     TELEPHONE: (202)463-7700
                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                  NAME: Cohen, Herbert REGISTRATION NUMBER: 25,109 REFERENCE/DOCKET NUMBER: 07
STRANDEDNESS
                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                        LENGTH:
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Linear

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ILOCATION: not available

IDENTIFICATION METHOD: experiment-
IDENTIFICATION METHOD: in specification
OTHER INFORMATION: prevention of IFN-2
OTHER INFORMATION: provoted cell death
PUBLICATION INFORMATION: not available
US-08-631-097-7
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ORIGINAL SOURCE:
ORGANISM: homo sa
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POSITION IN GENOME:
CHROMOSOME/SEGMENT: not applicable
MAP POSITION: not applicable
UNITS: not applicable
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LOCATION:
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CLONE: no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                       agagtactcgatacctgtgtttgacaacatgatgaaccgacacctagtagctcaagactt 2209
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                                                        CAACAACGTGCTGCCCGTCTTCGACAACCTGATGCAGCAGAAGCTGGTGGACCAGAACAT
                                                                                                                  CACCTTCATCGCAGCCAAGTTCGATGGCATCCTGGGCATGGCCTACCCCCGCATCTCCGT
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{\tt CTTCTCCTTCTACCTGAGCAGGGACCCAGATGCGCAGCCTGGGGGTGAGCTGATGCTGGG}
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Pred. No. 1e-19
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; SOFTWARE: PatentIn Ver. 2
; SEQ ID NO 11
; LENGTH: 2038
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-810-712-11
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Patent No. 6160106
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co. LTD
APPLICANT: Yeda Research and Development Co. LTD
TITLE OF INVENTION: Tumor Suppressor Genes, Proteins
TITLE OF INVENTION: Use of said Genes and Proteins
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 443; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: sequencelist CURRENT APPLICATION NUMBER: US/08/810,712G CURRENT FILING DATE: 1997-03-03 EARLIER APPLICATION NUMBER: PCT/US94/11598 EARLIER FILING DATE: 1994-10-12 NUMBER OF SEQ ID NOS: 31
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Pred. No. 1e-19;
0; Mismatches 378;
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APPLICANT: Tang, J. N.
                                     ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: ONRETELECOMMUNICATION INFORMATION:
TELEPHONE: 404-572-6508
            TELEFAX: 404-572-6555
INFORMATION FOR SEQ ID NO:
                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08090
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tang, J. TITLE OF INVENTION: TITLE OF INVENTION:
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                    FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                     CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                   STREET:
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; FEATURE:
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/organism="Bos taurus" /db_xref="taxon:9913" 11173 /note="unnamed protein product"	Location/Qualifiers 11173	Patent: WO 0114571-A 1 01 -MAR-2001; SemBloSys Genetics Inc. (CA)	van Rooijen, G., Keon, R.G., Boothe, J. and Shen, Y.	1 (bases 1 to 1173)	Bovidae; Bovinae; Bos.	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Bos taurus	COW.		AX088019.1 GI:13396947	AX088019	Sequence 1 from Patent WO0114571.	AX088019 1173 bp DNA linear PAT 17-MAR-2001	

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            gctgttactcacgctgctgagatcacccgcattcctctctacaaaggtaagtctctccgt
                                                  ATGAACTTCCTTAAGTCTTTCCCTTTCTACGCTTTCCTTTGTTTCGGTCAATACTTCGTT
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van Rooijen.G., Keon.R.G., Boothe,J.
Commercial production of chymosin in
Patent: WO 0114571-A 3 01-MAR-2001;
SemBioSys Genetics Inc. (CA)
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LFSVYMDRNGQESMLTLGAIDBSYYTGSLHWVPVTVQQYWQFTVDSYTISGVVVACEG
GCQAILDTGTSKLVGPSSDILMIQQAIGATQNQYGEFDIDCDNLSYMTTVFEINKM
YPLTPSAYTSQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDRANNLVGLAKAI"
9 790 c 609 g 1295 t
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1554. 2726
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/trans1_table=11
/protein_id="CAG34681.1"
/protein_id="CAG34681.1"
/db_xref="GI:13396950"
/trans1ation="MNELKSEPPYAFLCFGQYFVAVTHAAEITRIPLYKGKSLRKALK
/trans1ation="MNELKSEPPYAFLCFGQYFVAVTHAAEITRIPLYKGKSLRKALK
EHGLLEDFLOKQQYGISSKYSGFGEVASVPLTNYLDSQYFGKIYLGTPPQEFTYLFDT
GSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYGTGSMQGILGYDTVTV
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        aacaacctcgttgggctagctaaagcaatctga
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                                CAGAAATGGATCTTGGGAGATGTGTTCATTCGTGAGTACTACAGCGTCTTTGACAGGGCC
                                         cagaaatggatcttgggagatgtgtftcattcgtgagtactacagcgtctttgacagggcc
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Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence implies that this sequence might be a pseudogene mrna. or there may be an error in the cdna. the amino acid sequence deduced from this nucleotide sequence differs at three sites from bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chymosin is the major proteolytic enzyme in the fourth stomach of the unweaned calf. two chromatographically different forms, a at b, of the enzyme and its precursor are known and a third form, represented by this sequence, seems likely. the presence of a termination codon (bases 27-29) within the prepropeptide coding
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Bos taurus calf fourth
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Peo
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/db_xref="taxon:9913"
/tissue_type="fourth stomach mucosa"
/dev_stage="calf"
<1. 1269
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/protein_id="AAA30449.1"
/db_xref="GI:457097"
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Best Local Similarity
Matches 49; Conserv
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PATENT: JP 1983032896-A 1 25-FEB-1983;
BEPPU TERUHIKO
OS calf
PN JP 1983032896-A/1
PN JP 1983032896-
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                                                                                                        Patent: JP 1990109984-A 1 23
BEPPU TERUHIKO
OS BOVİNE
PN JP 1990109984-A/1
PD 23-APR-1990
PF 01-DEC-1988 JP 19883021
PI BEPPU TERUHIKO, UOZUMI
C12N15/59,C12N1/21;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC hypothetical: No;
CC *source: tissue_type=St
FH Key Linear;
FT CDS 1.108
PT CDS /produc
FT CDS /produc
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beppu, T., Uozumi, T. and Nishimori, K. COMPLEX PLASMID AND MICROORGANISM CONTAINING Patent: JP 1990109984-A 1 23-APR-1990;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
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  252
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01-DEC-1988 JP 1988302176
BEPPU TERUHIKO, UOZUMI TAKESHI, NISHIMORI KATSUHIKO
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/db_xref="taxon:32644"
                                                      /product=',
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/db_xref="taxon:9913"
327 c 300 g
                                             /organism="Bos taurus"
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         Wosnick, M.A.,
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Query Match 4.2%;
Best Local Similarity 100.0%;
Matches 49; Conservative
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M22593 M18758
M22593.1 GI:209139
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Mammalia; Eutheria; Cetartiodactyla; Ruminanti
Bovidae; Bovinae; Bubalus.
1 (bases 1 to 1101)
1 (bases 1, Mukhopadhyay, U.K., Mohanty, A.K.,
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                     synthetic construct artificial sequence.
1 (bases 1 to 1115)
                                                                                                                           prochymosin.
Synthetic DNA.
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/sub_species="bubalis"
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Barnett, R.W.,
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Pred. No.
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O; Mismatches
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7.5e-15;
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   Erfle, H.,
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   Elliott, R.,
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BASE COUNT
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Matches 49; Conserv
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Sequence 5 from Patent EP 012
104058
                                                                                                                                                                                                        AR002347
Sequence 2 from patent
AR002347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1175)
Cashion, L.M., McCaman, M.T., Rice, C.W. and Sias, S.R.
Recombinant DNA coding for a polypeptide displaying
                                                  Light-regulated promoters for produ
in filamentous fungi
Patent: US 5741665-A 2 21-APR-1998;
Location/Qualifiers
                                                                                                         1 (bases 1 to 1240)
Kato, E.K. and Stuart, W. Dorsey.
                                                                                                                                                 Unknown
                                                                                                                                                                                           AR002347.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown
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                                                                                                                                    Unclassified.
                                                                                                                                                                 Unknown.
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                                                                                                                                                                                                                                                                                                                                                        4.2%; Score 49;
larity 100.0%; Pred. No.
Conservative 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
356 c 318 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="synthetic construct"
/db_xref="taxon:32630"
332 c 302 g 227 t
            organism="unknown"
374 c 339 g
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1. .1115
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100.0%; Pred. No. 7.5e-15;
vative 0; Mismatches 0;
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US 5741665.
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0123928.
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7.4e-15;
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                                                                                           of heterologous proteins
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BOVCHYMOA
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Matches 49
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MEDLINE
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656 tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 704
                                                                           1 Similarity 100.0%; 149; Conservative 0;
                                                                                                                                                                        /product="chymosin a"
293 a 391 c 336 g
20 bases upstream from codon 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chymosin (rennin) is the major proteolytic enzyme in the fourth stomach of the unweamed calf. two chromatographically distinct forms are known and a third seems likely (see bovchymob and bovchymoc). this sequence has been tentatively identified as chymosin a; it differs from chymosin b by only two amino acids and from chymosin c by another amino acid. [1] argues that the different chymosins are probably polymorphic variants of a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 4.2%; S
l Similarity 100.0%;
49; Conservative 0;
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83054629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chymosin; chymosin A; rennin.
bovine (calf) cdna of fourth stomach mucosa mrna.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chymosin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moir,D., Mao,J.I., Schumm,J.W., Vovis,G.F., Taunton-Rigby,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus
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                                                                                                                                                                                                                                                                                      /codon_start=1
/protein_id="AAA30447.1"
/protein_id="AAA30447.1"
/protein_id="AAA30447.1"
/db_xref="GI 162858"
/db_xref="GI 162858"
/translation="MRCLVVLLAVFALSQGAETTRIPLYKGKSLRKALKEHGLLEDFL
/kranslation="MRCLVVLLAVFALSQYFGKIYLGTGYBQGILGYTDTGTSSDFWVPS
IYCKSWACKHHORFDDFRKSSTFQNLGKPLSIHYGTGSWQGILGYDTWTVSNILDIQQT
VGLSTQEPGGVFTYAEFDGILGWAYPSLASEYSIPVFDWMMNRHLVAQDLFSILDIQDT
VGLSTQEPGDVFTYAEFDGILGWAYPSLASEYSIPVFDWMMNRHLVAQDLFSILDTGT
SKLVGPSSDILNIQQAIGATQNQYDEFDIDCDNLSYMPTVVFEINGKMYPLTPSAYT
SQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDRANNLVGLAKAI"
                                                                                                                                                                                                                                     /note="presequence"
195. .1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="preprochymosin a"
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                                                                         4.2%; Score 49; DB
100.0%; Pred. No. 7.1
1ve 0; Mismatches
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a (rennin) mrna
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3. 7.3e-15;
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TITLE
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OS bovine calf
PN JP 1984021392-A/1
PD 03-FEB-1984
PF 30-JUN-1983 JP 1983119481
PR 01-JUL-1982 US 82 394433, 13-APR-1983 US 83 484539 PI
CHYYAARUSU EI BASURETSUTO
PC C12N15/00,C07H21/04,C12N1/20,C12P19/34,C12P21/02,(C12N15/00,
PC C12N1:19);
CC strandedness: Double;
CC topology: Linear;
CC topology: Linear;
CC topology: Linear;
CC anti-sense: No;
CC anti-sense: No;
CC anti-sense: No;
CC anti-sense: No;
CC mati-sense: No;
CC anti-sense: No;
CC anti-sense: No;
CC mati-sense: No;
CC anti-sense: No;
CC anti-sense: No;
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CC anti-sense: No;
CC mati-sense: No;
CC anti-sense: No;
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CC anti-sense: No;
CC anti-sense: No;
CC mati-sense: No;
CC anti-sense: 
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A15836
A15836.1 GI:48
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cDNA e
E00144
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                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos.
Bovidae; Bos.
1 (bases 1 to 1291)
51mons, A.F.M. and De Vos.W.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E00144.1 GI:2168443 JP 1984021392-A/1.
                                                                                                                             heterologous proteins
Patent: EP 0307011-A 5 15-MAR-1989;
NEDERLANDS INSTITUUT VOOR ZUIVELONDERZOEK
                                                                                                                                                                                                             DNA fragments, containing a lactic acid bacterium-specific regulator region for the expression of genes coding for no
                                                                                                                                                                                                                                                                                                                                                                                                                            COW.
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        323
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product='precursor polypeptide'.
Location/Qualifiers
1. .1289
                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:32644"
388 c 329 g
/db_xref="taxon:9913"
382 c 328 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="unidentified"
                                                      /organism="Bos taurus"
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Pred. No.
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Best Local S
Matches 49
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MEDLINE
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Best Local Similarity
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 654
 TGTTCTCGGTTTACATGGACAGGAATGGCCAGGAGAGCATGCTCACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bovine
J00003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harris,T.J.R., Lowe,P.A., Lyons,A., Thomas,P.G., Eaton,M.A.W., Millican,T.A., Patel,T.P., Bose,C.C., Carey,N.H. and Doel,M.T. molecular cloning and nucleotide sequence of cdna coding for calf
                                                                      l Similarity
49; Conserv
                                                                                                                                                            pst-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chymosin is the major proteolytic enzyme in the fourth stomach of the unweaned calf. two chromatographically different forms, a and b, of the enzyme and its precursor are known and a third form see likely (see bovchymoa, bovchymoc). this sequence has tentatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      been identified as coding for preprochymosin b. sequence comparison indicates that the precursors for chymosins a and b differ by only two amino acids, and for b and c by only four amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus
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bovine (calf) cdna
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                                                                    4.2%; Scilarity 100.0%; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Bos taurus"
/db_xref="taxon:9913"
<1. .1305</pre>
                                                                                                                                                                                                                                                                                                                                      /protein_id="AAA30448.1"
/protein_id="AAA30448.1"
/db_xref="G1:162860"
/translation-"MRCLYVLLAVFALSQGAEITRIPLYKGKSLRKALKEHGLLEDFL
/translation-"MRCLYVLLAVFALSQGAEITRIPLYKGKSLRKALKEHGLLEDFL
QKQQYGISSKYSGFGEYASVPLTNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDFWVPS
IYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYGTGSMQGILGYDTVTVSNIVDIQQT
                                                                                                                                                                                                                                                                                    VGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSIPVFDNMMNRHLVAQDLFSVYMDRN
GQESMLTLGAINPSYYTGSLHWVPVTVQQYWQFTVDSVTISGVVVACEGGCQAILDTG
TSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYMPTVVFEINGKMYPLTPSAYT
                                                                                                                                                                           /product="chymosin
393 c 340 g
                                                                                                                                                                                                                                                                  SQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDRANNLVGLAKAI'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="chymob mRNA" 26. .1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="preprochymosin b"
                                                                                                                                                                                                                               note="presequence"
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                                                                       Mismatches
                                                                                        . 49;
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3. 7.3e-15;
0;
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7.3e-1
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0;
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Best Local Similarity
Matches 49; Conserva
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                                             E00295
E00295.1 GI:2168583
JP 1985058077-A/3.
                                                                                                                      E00295 1460 bp cDNA encoding pre-prorennin A.
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Bos taurus
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peptide 278..1347
/product-'rennin'.
Location/Qualifiers
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440 c 398 g
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833 TGTTCTCGGTTTACATGGACAGGAATGGCCAGGAGAGCATGCTCACGCT 881
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JIERARUDO RARUFU FUINKU,
PI ARISON TAUNTON RIGUBII, ROBAATO JIENTORII NOURUTON, JIEN I
MAO, PI DONARUDO TEIRAA MOA, KURISUTOFUAA GOTSUDOBFURII GOFU PC
C12N15/00,C07H21/04,C07K13/00,C12N1/16,C12P21/02,(C12N1/16, PC
C12R1:865),
PC (C12P21/02,C12R1:865);
CC strandedness: Double;
CC strandedness: Double;
CC topology: Linear;
CC typothetical: NO;
CC *source: tissue_type=Stomach mucosa;
CC *source: tissue_type=Stomach mucosa;
CC *source: tissue_type=Stomach mucosa;
CC *source: clone=293-207 & 293-118/37;
FH Key
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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ALIGNMENTS

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 RESULT
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                  "Mature bovine chymosin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing chymosin in seeds of plants such as rice, flax, rape transforming plant cell with a nucleic acid encoding chymosin linked to transcription regulator and terminator sequences - \frac{1}{2}
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AC AAN3
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YFT CDS
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XX PN EP73
XX PN 02-1
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                                                                                                                                        Rennin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      aacaacctcgttgggctagctaaagcaatctga
                                                                                                                                                                                                                                                                                                                                                                 cagaaatggatcttgggagatgtgttcattcgtgagtactacagcgtctttgacagggcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atcttggataccggtacgtccaagctggtcggacctagcagcgacattctcaacattcag
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                                                                                                                                      renin;
                                                                                                                                                              of
                                                                                                                                                                                                                                          standard;
                                                                                                                                                              prorennin
                                                                                                                                                                                        (first
                                                                                                                                      enzyme;
                                                             Location/Qualifiers
1..1098
/*tag= a
                                                                                                                                                                                                                                          cDNA;
                                                                                                                                                                                     entry)
                                                                                                                                                              CDNA
                                                                                                                                     protease;
                                                                                                                                                                                                                                        1098
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                                                                                                                                                              pCR 10001
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RESULT
AAQ04683
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Best Local S
Matches 49
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               The inventors claim recombinant plasmids contg. the cDNA of calf prorennin. Specified plasmids are pCR 10001 and pCR2001 (contg. the whole sequence plus the lac promoter region). Also new are microorganisms transformed with the plasmids, esp. E. coli CR1 (ATCC 391710) contg. plasmid pCR2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-AUG-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid contg. calf microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-AUG-1981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Page 20-23; 32pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beppu T,
                                                                                                                                                                                                                                                                   05-OCT-1990
                                                                                                                                                                                                                                                                                                  AAQ04683 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BEPP/) BEPPU
                                                                                                                                                                                                                                                  Sequence encoding
                                Sequence 1098
                                                 plasmid
                                                                                       Complex plasmid and microbe - contains calf pro-rennin
                                                                                                                                                  01-JAN-1988;
                                                                                                                                                                   01-JAN-1988;
                                                                                                                                                                                                  JP02109984-A
                                                                                                                                                                                                                  Bos taurus
                                                                                                                                                                                                                                  Pro-rennin;
                                                                          Disclosure;
                                                                                                          P-PSDB;
                                                                                                                  WPI; 1990-168358/22.
                                                                                                                                 (BEPP/) BEPPU
                                                                                                                                                                                                                                                                                                                                         581 tgttctcggtttacatggacaggaatggccaggaggagcatgctcacgct 629
                                                                                                                                                                                                                                                                                                                                                   656 tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 704
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 49; Conserv
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                                                                                                          AAR05080.
                                                product may be pBR322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Uozumi T,
                                                                                                                                                                                                                                                                                                                                                                         4.2%; ilarity 100.0%; Conservative
                                                                          32;
                                                                                                                                                                                                                                  ds.
                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  BP;
                                  BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81JP-0131631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82EP-0107601
                                                                                                                                                   88JP-0302176
                                                                                                                                                                   88JP-0302176
                                                                         13pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                  252 A;
                                                                                                                                                                                                                                                   calf pro-rennin
                                  252 A;
                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pro:rennin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nishimori K;
 4.2%;
100.0%;
                                                        expressed
                                                                                                                                                                                                                                                                                                    1098
                                                                                                                                                                                                                                                                                                                                                                                                                   326 C;
                                  327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                           0;
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0; Mismatches
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  Score Pred.
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                                  300
                                                          in
49;
No.
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                                  G;
                                                          E.coli
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                                                                                                                                                                                                                                                                                                                                                                                                                    219
                                  219
                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
1e-14;
  DB 11;
1e-14;
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                                   Ή.
                                                          expression
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                                                                                                                                                                                                                                                                                                                                                                                                                    other;
                                    other
          Length 1098;
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                                                           system
                                                                                                                                                                                                                                                                                                                                                                            0;
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AAQ20949
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Best Local S
Matches 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cheese-making;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence encoding a polypeptide displaying milk clotting activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAN40295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAN40295
                                                                                                                                                                                      Also claimed is E.coli JM83/pLC7 (ATCC 39325) which is transformed with pLC7 contg. the prorennin derived sequence fused in phase with B-galactosidase. The pLC7 prorennin expression plasmid includes sequences which code for both the pseudorennin and mature rennin cleavage sites between AAs 28-29 and AAs 42-43, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                    sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
                                                                                                                                                                                                                                           Claim 6; Fig 2; 39pp; English.
                                                                                                                                                                                                                                                            Recombinant DNA coding for milk clotting polypeptide -expressed in transformed bacteria % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                        WPI; 1984-277277/45.
P-PSDB; AAP40559.
                                                                                                                                                                                                                                                                                                                    Cashion LM,
                                                                                                                                                                                                                                                                                                                                    (CODO-) CODON GENETIC ENG
                                                                                                                                                                                                                                                                                                                                                      31-MAR-1983;
                                                                                                                                                                                                                                                                                                                                                                        30-MAR-1984;
                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-1984.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      656
        13-MAY-1992
                         AAQ20949;
                                          AAQ20949
                                                                                                                                                                      Sequence 1175 BP;
                                                                                    5
                                                            6
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                                                                                                                           l Similarity 75.5
37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                   McCaman MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinant protein; rennet substitute; milk clot; ss
                                                                                                                                                                                                                                                                                                                                                                        84EP-0103551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 21..69
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                                                                                                                                                                      263 A; 355 C; 319 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA;
                                           cDNA; 1175
                                                                                                                                    4.2%;
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                                                                                                                                                                                                                                                                                                                     Rice
                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                            Score 49; DB 5;
Pred. No. 1e-14;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                     CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                     Sias
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                                                                                                                                                                        g;
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                                                                                                                                                                         0 other;
                                                                                                                             0,
                                                                                                                                             Length 1175
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                                                                                                                              Indels
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                                                                                          697
                                                                                                            704
                                                                                                                                                                                                                                                                          which
                                                                                                                                                                                                                    phase with
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                                                                                                                              Gaps
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RESULT
AAQ14051
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Best Local :
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                                                                                                                                                                                                                                                                                 specific clones were used to screen for recombinant plasmids. Only two clones 5G3 and 15C5 were found to contain the whole prorennin sequence with clone 5G5 having its complete coding sequence (shown here). The sequence was the same as the published sequence except for two silent mutations in codons 274 and 336 respectively, and a single mutation in codon 302 which converts the sequence to the B form of rennin. The product of prorennin, rennin is an active component of rennet which is used to clot milk in the process of making cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAY-1984;
12-DEC-1986;
31-MAR-1983;
28-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                        mRNA species, hybridisation with rennin specific probes was performed using probes derived from the published amino acid sequence of prorennin (Foltmann et al., J. Biol. Chem. 254, 8447-8456 (1979)) (see AAQ23291,2). Reverse transcriptase was used to transcribe mRNA into a cDNA copy which was inserted into plasmid pBR322 and cloned into E. coli strain K-12 MM 294 (ATCC 31446). The prorennin
                                AAQ14051 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolating heterologous polypeptide from bacterial inclusion bodies - by lysing cells, extn. with nonionic detergent and sepg. insoluble polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                           Sequence 1175 BP; 261 A; 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unweaned calf's stomach (abomasum). To identify rennin-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The prorennin (prochymosin) sequence was obtd.from mRNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McCaman MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BERL-) BERLEX LABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5082775-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prochymosin
                                                                                                         649
                                                                                                                    656 tgttctcggtttacatggacaggaatggccaggaagagcatgctcacgct 704
                                                                                                                                                                 Local Similarity
hes 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1992-049149/06.
DB; AAR20730.
                                                                                                    uguucucgguuuacauggacaggaauggccaggagagcaugcucacgcu
                                                                                                                                                                                                                                                                         AAQ20950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig 6; 21pp;
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    King JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (prorennin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84US-0609495.
86US-0940199.
83US-0480860.
86US-0856700.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= prorennin
/note= "also known ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autocatalytic activation; pseudorennin;
                               DNA; 1210
                                                                                                                                                                            4.2%;
75.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "also known as prochymosin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                 12;
                                                                                                                                                                              Score 49; DB 13
Pred. No. 1e-14;
                               ВP
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                                                                                                                                                                                                                                           319
                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                         <u>ଜ୍</u>
                                                                                                                                                                                                                                         240 U;
                                                                                                                                                                0;
                                                                                                                                                                                                                                         0
                                                                                                                                                                                             Length 1175;
                                                                                                                                                                                                                                         other;
                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    milk;
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                                                                                                                                                                                                                                                                                                   RESULT
AAT03006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          It was used as heterologous peptide/protein together with parts of the alpha-S1-casein gene in the prodn. of DNA constructs. The heterologous peptide or protein may also be human insulin-like growth factor I. The constructs provide high yields of the protein with simple recovery from the milk. Activation of the gene occurs only in the constructs.
10-MAY-1994;
                             09-MAY-1995;
                                                                                                                  Mammalian
                                                                                                                                                           al-3; albino mutant; light-regulated; Neurospora;
                                                                                                                                                                                          Chymosin open reading frame
                                                                                                                                                                                                                          13-JUN-1996
                                                                                                                                                                                                                                                      AAT03006
                                                                                                                                                                                                                                                                                     AAT03006 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1210 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 21; 41pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant DNA constructs for expressing protein in milk -contg. specific mammary gland transcription control region and signal sequence, providing high yield and easy prod. recovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP451823-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prorennin; alpha-S1-casein gene; insulin-like growth factor I; IGF-I; mammary gland; ss.
                                                          16-NOV-1995.
                                                                                      WO9530739-A1
                                                                                                                                                neterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1991-304858/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hartl P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CONE ) CONSORT ELEKTROCHEM IND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-APR-1990;
11-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mammary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                            656 tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct
                                                                                                                                                                                                                                                                                                                                                               643
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                            tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct
                                                                                                                                                                                                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ14050,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brem
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                gene; expression;
                                                                                                                                                                                                                        (first entry)
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94US-0240372
                             95WO-US05716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90DE-4012526
90DE-4011751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91EP-0105702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 A;
                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ14774-77
                                                                                                                                                                                                                                                                                                                                                                                                                                       4.2%;
100.0%;
                                                                                                                                                                                                                                                                                     1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356 C;
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 49; DB; Pred. No. 1e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                    ВР
                                                                                                                                                control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12;
1e-14;
                                                                                                                                                chymosin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 other;
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                                                                                                                                                            bread mould;
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                                                                                                                                                                                                                                                                                                                                                              691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mammary gland
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RESULT
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Best Local
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                                            Beppu T, Hidaka M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The DNA is that of a mammalian gene (open reading frame) encoding chymosin. The gene was placed in operable linkage with the al-3 promoter (see AAT03005). The al-3 gene controls the production of geranyl geranyl pyrophosphatase (GGPP) synthetase. GGPP is a precursor for carotenoids and xanthophylls. It has been shown that exposure to light increases the transcription level of GGPP synthetase 15-45 fold. Light activates a number of genes in the common bread mould, Neurospora. This can be used to regulate the expression of genes encoding heterlogous proteins, e.g. chymosin, in recombinant production systems. Use of a light-regulated promoter is a simple and effective way to control expression and allows timing to be adapted to the physiological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid for expression of heterologous protein - contains albino promoter for light induced expression in filamentous fungi
           P-PSDB; AAP40078
                      WPI; 1984-258001/42
                                                                                                      09-MAR-1983;
                                                                                                                            07-MAR-1984;
                                                                                                                                                    17-OCT-1984.
                                                                                                                                                                          EP121775-A.
                                                                                                                                                                                                            polyA_signal
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                                                                                                                                                                                                                                                                                                                                                                   AAN40055;
                                                                                                                                                                                                                                                                                                                                                                                          AAN40055 standard; DNA;
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                                                                                                                                                                                                                                                                                                                   Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYHA-) UNIV HAWAII.
                                                                                                                                                                                                                                                                                             Prochymosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                   700
                                                                                                                                                                                                                                                                                                                                                                                                                                                            656 tgttctcggtttacatggacaggaatggccaggaagagcatgctcacgct 704
                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                        taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                       Uozumi
                                                                                                                                                                                                                                                                                                                    prochymosin gene
                                                                                                                                                                                                                                                                                             expression vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 274 A; 374 C;
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1245..1250
                                                                                                      83JP-0038439
                                                                                                                             84EP-0102451
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                                                                                                                                                                                                                                                Location/Qualifiers
                                                        Nishimori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                          1278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                             E.coli trp operon; chymosin; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                        Shimizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16;
1e-14;
                                                       z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                       Kawaguchi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Best Local S
Matches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The inventors claim the prochymosin gene comprising a nucleotide sequence from (a) the 1st codon (GCT) to the 365th codon (ATC), or (b) the 5th codon (CGG) to the 365th codon (ATC); and recombinant plasmids harboured by Escherichia coli strains deposited as FERM BP-262, -263 and -264. Any portion of the nucleotide sequence as described in AAN40055 can be used. Also claimed is a vector derived from plasmid pBR322. Typically plasmid pCR501 is obtd. from pOCT 2. The transcriptional direction of pOCT 3 is opposite to that of pOCT 2; it is clockwise in pOCT 2 (5' to 3') whereas counter
         The inventors claim isolated chymosin (rennin) and prochymosin generation calves, and plasmids conty. the genes which are capable of replicating in a prokaryotic organism. The prokaryotic organism is pref. an Escherichia species, esp. E. coli p Gx 1225 (NRRL B-15061) The microorganisms transformed by the plasmid are also claimed.
                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                Isolated chymosin or rennin and prochymosin genes - which replicate in prokaryotic organisms, esp. Esche and organisms used for chymosin biosynthesis
                                                                                                                                                                                                                                  13-APR-1983;
01-JUL-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAN30022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAN30022 standard; DNA; 1289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression plasmid comprising prochymosin gene and vector useful for transforming Escherichia coli for prochymosin prodn
                                                                                         Claim
                                                                                                                                                                                                         (GENE-) GENEX CORP
                                                                                                                                                                                                                                                                                                   03-NOV-1983
                                                                                                                                                                                                                                                                                                                            BE897201-A
                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                 microbial vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Protolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence of veal chymosin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                    1983-820813/47.
DB; AAP30013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 4.2%;
l Similarity 100.0%;
49; Conservative (
                                                                                       Page 33-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
                                                                                                                                                                                                                                                                                                                                                                                                                                            enzyme; zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                 83US-0484539
82US-0394433
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1..1140
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                                                                                      43pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                         French.
                                                                                                                                                                                                                                                                                                                                                                                                                                             rennin; chymosin; cheese making;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49; DB 5;
Pred. No. 1e-14;
D; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                         plasmid(s)
                           (NRRL B-15061)
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RESULT 12
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AAN91157
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                                                                                   Query match
Best Local Similarity
Matches 49; Conserv
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Best Local
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                                                                                                                                                     The DNA encoding prochymosin can be cloned into a plasmid (esp. fros. cremoris SK112) and used to produce large amts of the protein by recombinant DNA techniques. This could overcome the shortage of prochymosin due to shortage of calf stomachs and increasing cheese prodn. Prochymosin is also used in prodn. of yoghurt, butter and buttermilk. See also AAN91158-N91160.
  AAN30049 standard;
                                                                                                                                                                                                                                        DNA fragment having region specifi is contained in plasmid in microor protein and food prodn. eg cheese.
                                                                                                                                     Sequence
                                                                                                                                                                                                                        Disclosure; fig 2; 43pp; Dutch.
                                                                                                                                                                                                                                                                                          WPI; 1989-030097/04.
                                                                                                                                                                                                                                                                                                              Simons
                                                                                                                                                                                                                                                                                                                                                                      12-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                precursor_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cloned sequence of (pro)chymosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1990 (first entry)
                                                                                                                                                                                                                                                                                  P-PSDB;
                                                                                                                                                                                                                                                                                                                                 (NEZU-) NEDERL INS ZUIVELON
                                                                                                                                                                                                                                                                                                                                                   12-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                        02-JAN-1989
                                                                                                                                                                                                                                                                                                                                                                                                          NL8701378-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAN91157 standard; DNA; 1291 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                        656 tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactic acid
                                                 609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         656 tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                              tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.2%;
11 Similarity 100.0%;
49; Conservative (
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                                                                                                                                    1291 BP;
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                                                                                   4.2%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
29. 1123
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                              /product-;prochymosin
                                                                                                                                    323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310
  cDNA;
                                                                                                                                                                                                                                                                                                              X
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                                                                                                                                    Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cheese; Streptococcus
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                                                                                                                                    385
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                                                                                                                                                                                                                                                 specific for lactic acid bacteria microorganism used in prodn. of
                                                                                    0;
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                                                                                   Score 49; DB 10;
Pred. No. 1e-14;
0; Mismatches
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Pred. No.
  ВP
                                                                                                                                   326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                   G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ი;
                                                                                                                                   257
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1e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cremoris SK112; chymosin;
                                                                                    0;
                                                                                                                                   0 other;
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                                                                                                     Length 1291;
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                                                                                   Indels
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                                                                                                                                  RESULT 13
AAN20043
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                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                            Preprochymosin is an intermediate (via prochymosin and pseudochymosin) for the enzyme chymosin, which is the essential milk-clotting component of rennet and is used in cheese manufacture. AAN30049 corresp. to mRNA isolated from the fourth stomach of a preruminant calf (abomasum, Frisian cow).
Key
                                                                                                                                                                                                                                                                                                                                                        DNA molecules comprising genes for preprochymosin - ustransform microorganisms to give strain producing the prepro-enzyme and its allelic and maturation forms
                   Bos taurus
                                   Pre-pro-rennin; rennin;
protease; milk-clotting
                                                                Pre-prorennin-A gene DNA sequence.
                                                                                                     AAN20043;
                                                                                                                        AAN20043 standard; DNA;
                                                                                                                                                                                                                                                           Sequence 1314 BP;
                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1983-39656K/17.
P-PSDB; AAP30086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP77109-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA sequence
                                                                                   16-DEC-1992
                                                                                                                                                                   Maat J,
                                                                                                                                                                                                                                                                                                                                                                                                                                               (UNIL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-OCT-1981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-OCT-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-APR-1983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chymosin; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bovine preprochymosin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAN30049;
                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                      2; Fig 1; 53pp; English.
                                                                                                                                                                                                            l Similarity
49; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                               UNILEVER NV
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llarity 100.0%;
Conservative (
                                                                                 (first entry)
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41..1169
Location/Qualifiers
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                                                                                                                                                                                                                                                           309 A;
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                                                                                                                        1460
                                    prorennin; enzyme;
enzyme; ss.
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                                                                                                                                                                                                                                                           398 C; 338 G; 269 T;
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                                                                                                                                                                                                            0;
                                                                                                                                                                                                                     Score 49;
Pred. No.
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                                                                                                                        ВР
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                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           Edens
                                                                                                                                                                                                                     DB 4;
1e-14;
                                             EC-3.4.23.4;
                                                                                                                                                                                                                                                           0 other;
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RESULT 1
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Best Local S
Matches 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
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16-JAN-1981;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
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                                                                           03-OCT-1984.
                                                                                                GB2137208-A.
                                                                                                                                                                                             Yeast
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                                                                                                                                                                                                                                      25-JAN-1992
                                                                                                                                                                                                                                                                                AAN40180 standard;
            (COLB ) COLLABORATIVE RES INC
                                 28-FEB-1983;
                                                     28-FEB-1984;
                                                                                                                                                                                                                                                                                                                                    833
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                                                                                                                                                                                             expression
                                                                                                                                                                                                                                                                                                                                                                            ch 4.2%;
l similarity 100.0%;
49; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Table 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells producing rennin and its precursors - recombinant {\tt DNA} material
                                                                                                                                                                                                                recombinant CGF4
                                                                                                                                                                                                                                      (first entry)
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81US-0225717.
                                 83US-0470911.
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/*tag= a
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205..1350
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/note= "pre-prorennin-A gene"
                                                                                                                                                                                             vector; GAL1 promoter; Saccharomyces cerevisiae;
                                                                                                                                                                                                                                                                                CDNA; 1460
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0; Mismatches
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1e-14;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The inventors claim a DNA segment contg. GAL1 promoter linked to gene - useful for direction of expression of the gene in yeast. The recombinant material carrying a GAL1 promoter of the yeast galactokinase gene may be used in expressing a desired protein, bovine growth hormone, interferon, prorennin or preprorennin, in yeast cell. Strains of Saccharomyces cerevisiae producing the polypeptides are produced. Yeast strains deposited as ATCC 2064: 20661, 20662 and 20663, strain designations CGY 196, 457, 461 and 20663.
  BamHI/SalI insert,
                                             Disclosure; ;
                                                                                                             Kluyveromyces host cells for producing polypeptide(s) used for highly efficient prodn. of eg chymosin tissue
                                                                                                                                                                                                                                                  van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP301670-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1460 BP; 328 A; 440 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Table 4, Page 21-23; 35pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               direction of expression
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Mao JI, Moir DT, Gof
                                                                                                                                                                                P-PSDB;
                                                                                                                                                                                                                                                                                         (KONN ) GIST-BROCADES NV
                                                                                                                                                                                                                                                                                                                                                                                28-JUL-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kluyveromyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kluyveromyces;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-1990
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                                                                                                                                                                                                                                                  den Berg
                                                                                                                                                                                1989-033565/05.
DB; AAP94376.
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                                                                                      activator or
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                                             56pp;
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incorporated
                                             English.
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CG;
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                                                                                           human
                                                                                                                                                                                                                                                    AJJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB 5;
Pred. No. 1e-14;
0; Mismatches
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into plasmids pAB309
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                                                                                                                                                                                                                                                    Rietveld
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promoters, terminators and a G418 resistance marker fused to a ADH1 promoter from S.cerevisiae.

The Kluyveromyces expression systems provide highly efficient secretion and processing of a wide variety of proteins.

Sequences identical to those published in EP301669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2727 BP; 752 A; 654 C; 572 G; 749 T; 0 other;
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Maximum DB seq length: 2000000000
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

   Match
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  GenCore version 4.5
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AA411567 zv2zg01.s
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Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agrifor, Dept of AFNS, U of A, E
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                sequence.
BG938086
BG938086.1
                                                                                                                                                                                                                                                                                                                                           BG938086
1Abo11A08
                                                                                                              Email: smoore@afns.ualberta.ca
The sequence best matches qb:BPU19786 (Bos primigenius prochymosin mRNA, complete cds) in main database at high score of 735.0 and E-value of 0.0
PCR PRimers
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Moore, S.S., Hansen, C., Li, C.
cDNA's from bovine abomasum
                                                               High quality sequence stop: POLYA=No.
                                                                         BACKWARD: M13 Reverse
Seq primer: T3 primer
High quality sequence
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Bovidae; Bovinae; Bos.
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/db_xref="taxon:9913"
/clone_1ib="Bovine Abomasum cDNA Library"
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49; Conser
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Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                      Seq primer: T3 primer 
High quality sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia: Pecora: Roucidos
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larity 100.0%;
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I; Site_2: Xho I"
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I; Site_2: Xho I"
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Mammalia; !
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49; Conserv
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 472)
Moore, S.S., Hansen, C., Li, C., Fu, A.
cDNA's from bovine abomasum tissue
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovinae; Bos. 1 (bases 1 to 399)
                                                                                            EST.
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The sequence best matches gb:BOVCHYMOA (bovine chymosin a (rennin)
mrna) in main database at high score of 928.0 and E-value of 0.0
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High quality sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Epithelial"
/dev_stage="Young adult"
/lab_host="XII-BlueMRF'-strain"
/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
143 c 131 g 94 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Bos taurus"
/db_xref="taxon:9913"
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thes 0;
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CDNA 5', mRNA
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                                  Bovoidea;
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Best Local
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nes 43; Conserv
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Arabidopsis thaliana
Arabidopsis; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (base; 1 to 325)
1 (base; 1 to 325)
1 (base; 1 to 325)
                                                                                                                                                                                                      A large scale analysis of cDNA in Arabidopsis thaliana: of 12,028 non-redundant expressed sequence tags from nor size-selected cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                              AV532492 325 bp mRNA linear AV532492 Arabidopsis thaliana flower buds Columbia thaliana cDNA clone FB043b03F 3', mRNA sequence. AV532492
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                          The First Laboratory for Plant Gene Research Kazusa DNA Research Institute
                                                                                                                                                                    DNA Res. 7, 175-180 (2000)
20363093
                                                                                                                                                                                                                                                                                                                                                                                                             AV532492.1 GI:8692775
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                                                                        Yana 1532-3, Kisarazu, Chiba
Email: asamizu@kazusa.or.jp,
                                                                                                                                                   Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLYA-No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: smoore@ains.ualberta.ca
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   /organism="Arabidopsis thaliana"
/strain="Columbia"
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/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Two males and one female mixed" /tissue_type="Gastrointestinal tissue /cell_type="Epithelial"
                                                       Location/Qualifiers
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0; Mismatches
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                                                                        URL:http://www.kazusa.or.jp/en/plant/.
                                                                                             292-0812, Japan
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. 5.3e-11;
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EST.
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MSU-DOE Plant Research Laboratory
Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95148729
On Jan 7, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 517-353-0854
Fax: 517-353-9168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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2911 Lambda-PRL2 Arabidopsis
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                    67
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            /clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_2: Not;
/note="Vector: lambda Zip-Lox; The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA."

67 a 61 c 92 g 106 t 13 others
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/clone_lib="Arabidopsis thaliana flower buds Columbia"
/tissue_type="flower buds"
                                                                                                                                                                                                                                                                          /organism="Arabidopsis
/strain="var columbia"
/db_xref="taxon:3702"
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100.0%; Pr
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Pred. No. 1.1
0; Mismatches
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Score Pred.

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AV538262 Arabidopsis thaliana roots Col
cDNA clone RZ113a03F 3', mRNA sequence.
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1 (bases 1 to 380)
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l Similarity 100.0%;
23; Conservative
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                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 391) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Pro
                                                                                                                                                                                                                                                                                                                                                        AA969042 391 bp mRNA linear EST 07-JUL-19
op43d07.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1579597 3' similar to TR:Q27951 Q27951 PROCHYMOSIN. ;, mRNA
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l: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="RZ113a03F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Arabidopsis thaliana roots Columbia"
/tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
IMAGE Consortium (info@image.llnl.gov) for further information.
IMAGE CONSORTIUM (info@image.llnl.gov) for further information.
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zv22g01.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IM.
similar to SW:CHYM_SHEEP P18276 PROCHYMOSIN PRECURSOR,
                                                                                                                                                                                                                                                                                                                                                                                               Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
washU-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
AA411567
AA411567.1 GI:2069151
                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seg primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 374.
                                                                                                                                                                                                                                                         Washington University Scho
4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
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/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                   /organism="Homo sapiens"
                                                                     Location/Qualifiers
                                                  . 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                            school of Medicine
way, Box 8501, St. !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9;
1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 391;
                                                                                                                                                                                                                                                                                                                            Louis, MO 63108
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Indels

0;

Gaps

0

IMAGE:754416

B-FORM

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REFERENCE
AUTHORS
TITLE
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AV518232/c
  BASE COUNT
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MEDLINE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                        A large scale analysis of cDNA in Arabidopsis thaliana: Generati of 12,028 non-redundant expressed sequence tags from normalized size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
23; Conserv
                                                                                                                                                                                                                                                                        The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AV518232
AV518232 Arabidopsis thaliana at old Arabidopsis thaliana cDNA clarations
                                                                                                                                                                                                                                                                                                                                                                Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                         20363093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 408)
    135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
    D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR amplified cDNAs from pools of ,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 34048B-345479, and 48448B-489479."
                        XhoI
                                                                                                        /clone_lib="Arabidopsis thaliana aboveground
six-week old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pregnant uterus"
                                                              /tissue_type="aboveground organs"
/dev_stage="two to six-week old"
                                                                                                                                                /organism="Arabidopsis
/strain="Columbia"
/db_xref="taxon:3702"
/clone="APDI3d01F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GDB:5977315"
/db_xref="taxon:9606"
/clone="InAGE:754416"
/clone_lib="Soares_NhHMPu_S1"
                                       note="Vector: pBluescriptII SK-;
                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: mixed (see below); Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Pooled human melanocyte, fetal heart,
    112 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.0%;
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Pred. No. 1.2;
69 g
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    92
                                                                                                                                                                                                                thaliana'
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                                          Site_1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
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                                       EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to six-week
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                                                                                                                            organs
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VERSION KEYWORDS

ACCESSION

SDSO

SOURCE

FEATURES

Query Match

Score

23;

DB

9;

Length

408;

COMMENT

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ORIGIN

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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                              ACCESSION
VERSION
                                                                                                                                                                                                                     RESULT :
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AUTHORS
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KEYWORDS
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AV559941/c
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                                                           REFERENCE
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ORIGIN
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                                                                                                                                                                                        DEFINITION
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MEDLINE
                                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                      Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                            1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285
                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tggatcttgggagatgtgttcat 1109
                                                                                                                                                                         zv22g01.rl
similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AV559941 411 bp mRNA linea
AV559941 Arabidopsis thaliana green siliques Col
thaliana cDNA clone SQ126c01F 3', mRNA sequence.
AV559941
1 (bases 1 to 438)
Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,
Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
Mammalia;
                                                                                                                                 _{\rm TSH}
                                                                                                                                                                                                         AA411566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The First Laboratory for Plant Gene Research Kazusa DNA Research Institute
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20363093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 411)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
                                                                                                    Homo sapiens
                                                                                                                                              AA411566.1
                                                                                                                                                              AA411566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV559941.1 GI:8731367
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                                                                                                                                                                                                                                                                                                                                                                                                                               136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db.xref="taxon:3702"
/clone="SQ126c01F"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis
/strain="Columbia"
                                                                       ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBluescriptII
                                                                                                                                                                    438 bp mRNA linear EST 17-MAY-19 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:754416 TR:G457097 G457097 CHYMOSIN C. [1];, mRNA sequence.
                                                                                                                                               GI:2069150
                                                                                                                                                                                                                                                                                                                                                    2.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                             109
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                                                                       Chordata;
Primates;
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                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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s Columbia Ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from normalized and
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IMAGE:754416 5'
                                                                                                                                                                                                                                                                                                                                      0;
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COMMENT
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AV536021/c
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Best Local Similarity
Thehes 23; Conservi
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JOURNAL
                                                                                                                                                                                                                                                                        AUTHORS
TITLE
                                                                                                                                                                               JOURNAL MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
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                                                                                                                                                                                                                                                                   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases I to 483)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV536021
AV536021.1 GI:8696304
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                                                                                                           Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                               DNA Res. 7, 175-180
20363093
                                                                                                                                                                                                                           of 12,028 non-redundant expressed sequence tags from normalized size-selected cDNA libraries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
                                                                 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polyylnker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and scircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
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/clone="IMAGE:754416"
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/db_xref="GDB:5977315"
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/organism="Arabidopsis thaliana"
                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
IMAGE Towarth: 608 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A1479358 The tm27e07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157828 3' similar to TR:Q28950 Q28950 PREPROCHYMOSIN
  23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 505)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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2.0%;
ilarity 100.0%;
Conservative
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                                                                                                             / note "Dogan: pooled; Vector: pT7T3D-Pac (Pharmacia) with /note "Organ: pooled; Not I; Site_2: Eco RI; a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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/tissue_type="flower buds"
/tissue_type="flower buds"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
ybc!"
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                      Score 23;
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  Indels
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1015 ccctccgcctataccagccagga 1037

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271 CCCTCCGCCTATACCAGCCAGGA 249

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VERSION
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AV518638/c
LOCUS
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AUTHORS
TITLE
Search completed: July 31, Job time: 17275 sec
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Best Local Similarity 100.0%;
Matches 23; Conservative (
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S EST.

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ISM Arabidopsis thaliana cDNA clone phyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. CE 1 (bases 1 to 511)

RS Asamizu,E. Nakamura,Y., Sato,S. and Tabata,S. A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries

AL DNA Res. 7, 175-180 (2000)

NE 20363093

Contact: Erika Asamizu

The First Laboratory for Plant Gene Research

Kazusa DNA Research Institute

Yana 152-3, Kisarazu, Chiba 292-0812, Japan

Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.

Erica 1. 511
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                                                                                                                                                                                                                                                                                                                                                                                        /organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                "Iodx
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/dev_stage="two to six-week old"
/note="Vector: pBluescriptII SK-;
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              2002, 23:07:30
                                                                                                                                                                        0; Mismatches
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Pred. No. 1.2;
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Result
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                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
         Score
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3957
1 ctgcaggaattcatt
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KEYWORDS
SOURCE
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AX088021
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1 (bases 1 to 3957)
van Rooijen,G., Keon,R.G., Boothe,J. and Shen,Y.
Commercial production of chymosin in plants
Patent: WO 0114571-A 3 01-MAR-2001;
SemBioSys Genetics Inc. (CA)
Location/Qualifiers
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Sequence 3 from Patent WO0114571.
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Phaseolus vulgaris. Phaseolus vulgaris RESULT 2
PHVBCSP
LOCUS
DEFINITION

PHVBCSP 3502 bp DNA linear PLN 17-JUN-1998 Phaseolus vulgaris beta-type phaseolin storage protein gene, complete cds. J01263 M13758 J01263.1 GI:3228361

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TATAA 3060	CAATTCTAACTTTAGCATTGTGAACGAGACATAAGTGTTAAGAAGACATAACAAT	3001	DЬ

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Submitted (27-APR-1993)
Station, TX 77843-3155,
4 (bases 1 to 3502)
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The glycosylated seed stor
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On Jun 16, 1998 this sequence version replaced
Location/Qualifiers
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2791. .3049,3153. .3367)
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EGALFVPHYYSKAIVILVVNEGEAHVELVGPKGNKETLEYESYRAELSKDDVFVIPAA
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PVNNPQIHEFFLSSTEAQQSYLQEFSKHILEASFNSKFEEINRVLFEEEEGQQEEGQQE
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Chordata; Craniata; Vertebrata; Cetartiodactyla; Ruminantia; Peo
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1 (bases 1 to 1173)

van Rooijen,G., Keon,R.G., Boothe,J.
Commercial production of chymosin in
Patent: WO 0114571-A 1 01-MAR-2001;
SemBloSys Genetics Inc. (CA)
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FINANCIAN CONTROL OF THE CANALY OF THE CATALYCTY
GSSDFWYPSIYCKSAACKNHQREDFRKSSTFQNLGKPLSIHYCTGSMOGILGYDTYTY
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308 c 262 g 304 t
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TACTCGATACCTGTGTTTGACAACATGATGAACCGACACCTAGTAGCTCAAGACTTGTTC

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Phaseolus vulgaris

Eukaryota; Viridiplantae; Strep
Spermatophyta; Magnoliophyta; e
Rosidae; eurosids I; Fabales; F
Phaseolus.

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Sequence 5 f:
AX343913
AX343913.1
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Heterologous gene expression in plant
Patent: WO 0200899-A 5 03-JAN-2002;
Vlaams Interuniversitair Instituut vo
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/organism="Phaseolus
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Jung, R. and Kinney, A.J.
Hypoallergenic transgenic soybeans
Patent: WO 0168887-A 2 20-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                        synthetic construct
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INTERNATIONAL, INC. (US)
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/note="chimeric construct"
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               DEVELOPMENT OF PLANT STRUCTURAL GENE
DEVELOPMENT OF PLANT STRUCTURAL GENE
PATENT: JP 1985210988-A 2 23-OCT-1985;
AGURIJIENETEIKUSU RES ASSOC LTD
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PN JP 1985210988-A/2
PD 23-OCT-1985
PF 16-APR-1984 JP 1984077452
PF 16-APR-1983 US 83 485614
PI JIVON DELI KENPU, TEIMOSHII SHII HOC
DENISU DABURITU SARSUTON, NORIMOTO PC
C12R1:91);
CC C12R1:91);
CC strandedness: Double;
CC c12R1:91);
CC strandedness: Double;
CC topology: Linear;
CC topology: Linear;
CC topology: Linear;
CC anti-sense: No;
CC anti-sense: No;
CC anti-sense: No;
CC atti-sense: No;
CC TS TS UTR
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FT 5'UTR
11768. 1958)
FT 1768. 1958)
FT 1768. 1958)
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                   Norimoto, M
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15-APR-1983 US 83 485614
JIYON DEII KENPU, TEIMOSHII SHII HOORU, JIERII
DENISU DABURIYU SATSUTON, NORIMOTO MURAI
                                                                                                                                                                                      C12N15/00, A01H1/00, C12N1/20, C12N5/00, (C12N1/20, C12R1:01),
promoter
                                                                                         *source: library=plasmid pKS4-KB;
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             Teimoshii, S.H.,
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                                  .753,842. .922,1047.
/product='faseorin
101. .177
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                                  .1664,
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Best Local Similarity
Matches 181; Conserv
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Artificial sequence
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1 (bases 1 to 2090)

Kemp,J.D., Hall,T.C., Slightom,J.L.,

Plant structural gene expression

Patent: EP 0126546-A 24 28-NOV-1984;

LUBRIZOL GENETICS INC.
                                                                                                                                                                           synthetic construct. synthetic construct
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                                                        /organism="synthetic construct"
/db_xref="taxon:32630"
join(178. .490,563. .753,842. .91768. .1958)
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416 c 372 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
       /transl_table=11
/product="phaseolin"
/protein_id="CAA00562.1"
/db_xref="GI:490412"
                                                                                                       Location/Qualifiers
translation="MMRARVPLLLLGILFLASLSASFATSLREEEESQDNPFYFNSDN/
                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1665. .1767
/note='iVS5,103bp'
1768. .1958
1958. .<2090.
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842. .922
923. .1046
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1047. .
1278. .
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Pred. No. 9.9e-77;
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phaseolin.
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. .1277
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                                                                                      Phaseolus vulgaris gene for alpha-phaseolin. x52626 x52626 x52626.1 GI:20972 alpha-phaseolin; glycoprotein; phaseolin; seed storage protein. phaseolus vulgaris. Phaseolus vulgaris Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; spermatophyta; Magnoliophyta; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Posidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Anthony,J.L.
Direct Submission
Submitted (17-APR-1990) Antony J.L., Dept. of Biology,
University, College Station, TX 77843-3258, USA
2 (bases 1987 to 4764)
                                                                              Phaseolus.
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llarity 100.0%;
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923..1046
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/number=2
842. .922
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491. .562
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RSGSALIVLVKPDDRREYFFLTSDNPIFSDHQKIPAGTIFYLVMPDPKEDLRIIQLAM
PVNNPQIHEFFLSSTEAQQSYLQEFSKHILBASFNSKTEELINRVLFEEBEQQEEVIVU
IDSEQIKELSKHAKSSSRKSLSKQDNTIGNEFGNLTERTDNSLNVLISSIEMEEGALF
VPHYYSKAIVILVVNEGEAHVELVGPKONKETLEYESYRAELSKDDVFVIPAAYEVAI
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754..841
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1665. .176
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1278. .14
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423 c
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1768. >1958
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Pred. No. 9.8e-77;
0; Mismatches 0;
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Matches 269;
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CATGCATGTTCCAACCACCTTCTCTCTTATATAATACCTATAAATACCCCTAATATCACT
                                                                      aatttottcacttcaacacacgtcaacctgcatatgcgtgtcatcccatgcccaaatctc 1406
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nilarity 99.3%;
Conservative
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4084. .4137
/note="repeat region"
a 897 c 782 g
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/translation="MMRARVPILLLGILFLASLSASFATSLRBEEESQDNPFYFNSDN
SWNTLFKNYGVGHIRTLGFEFOQDSKRLQNLEDYRLVEFRSKPETLLLPQQADAELLLVV
RSGSAILVLVKPDDRREYFFLTSDNPIFSDHQXIPAGTIFYLVNPDPKEDLRIIQLAM
PVNNPQIHDFFLSSTEAQOSYLQEFSKHILEASFNSKFEEINEVLFAREGQDEGVIVN
IDSEQIEELSKHAKSSFKSLSKQDNTIGNEFOLITERTDNSLNVLISSEMKEGALF
VPHYYSKAIVILVVNEGEAHVELVGPKONKETLEYESTRAELSKDDVFYIPAAYPVAI
KATSKVNFTGFGINANNNRKLLAGKTDNVISSIGRALDGKDVLGLTFSGSGEEVMKL
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3580. .38
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3221. .34
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2352. .2417
2665. .2736
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/protein_id="CAA36853.1"
/db_xref="GI:295832"
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2196. .2207
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..3838,3942..4159)
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                                                                                                                                                                                                                                                                                                                                      .>4159
                                                                                                                                                                                                                                                                                                                                                                   .3941
                                                                                                                                                                                                                                                                                                                                                                                                                                 .3579
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                                                                                                                                                                                 0;
                                                                                                                                                                              Score 169; DB 8; Length 4764; Pred. No. 6.2e-71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2927,3016. .3096,3221.
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                                                                                                                                                                              Gaps
                                                        2204
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PVPHASBR
LOCUS
                                                             ACCESSION
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ACCESSION
VERSION
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LOCUS
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Best Local Sim
Matches 133;
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TITLE
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                                                                                                                                                                                          aggatgttatgat 2864
                                                                                                                                                                                                                                                                                                                   aataagtatgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgt 2791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthetic construct.

w synthetic construct
artificial sequence.
1 (bases 1 to 1475)
1 (bases 1 to 1475)
Remp.J.D., Hall.T.C., Slightom,J.L., Su
Plant structural gene expression
Patent: EP 0126546-A 33 28-NOV-1984;
LUBRIZOL GENETICS INC.
                                                                                                                                                                          AGGATGTTATGAT 1475
                                                                                                                                                                                                                                                                                                    AATAAGTATGAACTAAAATGCATGTAGGTGTAAGAGCTCATGGAGAGCATGGAATATTGT 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAACTCATATTCAATACTACTCTACTATGA 2355
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                                                                                                                                                                                                                                     ATCCGACCATGTAACAGTATAATAACTGAGCTCCATCTCACTTCTTCTATGAATAAACAA 1462
                             x03004.1 GI:21039 glycoprotein; phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Artificial mRNA for phaseoline.
A11822
A11822.1 GI:491197
storage protein.
Phaseolus vulgaris
                                                             Phaseolus vulgaris mRNA X03004
                                                                                              PVPHASBR
                                                                                                                                                                                                                                                                                                                                                               h 3.4%;
Similarity 100.0%;
33; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /Translation="MMRRRYPLLLLGILFLASLSASFATSLREEEESODNPFYFNSDN
SWNTLFKNQYGHIRVLQRFDQQSKRLQNLEDYRLVEFRSKPETLLLPQQADAELLLVV
RSGSALIVLVKFDDRREYFFLYSDNP1FSDHQXIPAGTIFYLVHDDPKEDLR1IQLAM
PVNNPQIHEFFLSSTEAQQSYLQEFSKHILEASFNSKFEEINRVLFEEEGQQEGVTV
IDSEQIXELSKHAKSSSRKSLSKQDNTIGNEFGNLTERTDNSLNVLSSIEMEEGALF
VPHYYSKAIVILVVNEGEAHVELVGPKGNKETLEYESYRAELSKDDVFVIPAAYPVAI
KATSNVNFTGFGINANNNNRNLLAGKTDNVISSIGRALDGKDVLGLTFSGSGDEVMKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               INKQSGSYFVDAHHHQQEQQKGRKGAFVY"
334 c 306 g 380 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="phaseoline"
/protein_id="CAA00988.1"
/db_xref="GI:491198"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
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78. 1343
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                             phaseolin;
                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                               Score 133; DB 6;
Pred. No. 2.6e-53;
0; Mismatches 0;
                                                                            for beta-type
                                                                                              1475
                             seed storage protein; signal peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                            ďď
                                                                          mRNA linear
pe phaseolin.
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                                                                                                                                                                                                                                                                                                                                                                                             Length 1475;
                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                          PLN
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REFERENCE
AUTHORS
TITLE
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                                                                                                            Query Match
Best Local S
Matches 133
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                                                1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sig_peptide
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                                                                               2732
                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                 variation
                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                          Local Similarity
                                             atccgaccatgtaacagtataataactgagctccatctcacttcttctatgaataaacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phaseolus vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The single base deletion in a variant clone can be due cloning artefact or to a represented pseudogene.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Slightom,J.L., Drong,R.F., Klassy,R.C. and Hoffman,L.M. Nucleotide sequences from phaseolin cDNA clones: the major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phaseolus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 13 (18), 6483-6498 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins from Phaseolus vulgaris are encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amilies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 1475)
                                                                                                                                                                                                         455
                                                                                                          3.4%; Score 133; DB 8; ilarity 100.0%; Pred. No. 2.6e-53; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SWISS-PROT: P02853"
/translation="mmrarvplilligitelasisasfatslreeeesqdnpfyfnsdn
/translation="mmrarvplilligitelasisasfatslreeeesqdnpfyfnsdn
Swntlfknqyghirvlqafedqoskrlqnledyrlvefrskfpetilliqlam
rsgsatlvlvkpddrreyffitsdnpifsdhqxipagtifylnyddfeeegqdedyin
pynnpqihefflssteaqosylqefskhileasfnskfeeinrylfeeegqdedyin
                                                                                                                                                                                                                                      /note="put.
1475
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KATSNVNFTGFGINANNNNRNLLAGKTDNVISSIGRALDGKDVLGLTFSGSGDEVMKL
INKQSGSYFVDAHHHQQEQQKGRKGAFVY"
                                                                                                                                                                                                                                                                                                                                                                               /note=
170
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="
152. .1
                                                                                                                                                                                                      /note="polyadenylation site"
335 c 306 g 379 t
                                                                                                                                                                                                                                                                                                                                  and premature stop 831. .839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="mature beta-phaseolin (aa 1-398)"
149. .150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAA26789.1"
/db_xref="GI:21040"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Phaseolus vulgaris"
/db_xref="taxon:3885"
                                                                                                                                                                                                                                                                      1454. .1458
                                                                                                                                                                                                                                                                                                     1098.
                                                                                                                                                                                                                                                                                                                                                               /note="A is missing
                                                                                                                                                                                                                                                                                                                                                                                                            /note="pot. altern. signal
155. .156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="cap site in variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="mRNA"
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                                                                                                                                                                                                                                                                                   1098. .1106
/note="pot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDSEQIKELSKHAKSSSRKSLSKQDNTIGNEFGNLTERTDNSLNVLISSIEMEEGALF
                                                                                                                                                                                                                                                                                                                    'note="pot.
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.153
                                                                                                                                                                                                                                                                                                                                                                                              pot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     putative"
                                                                                                                                                                                                                                                                                                                  glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                              altern.
                                                                                                                                                                                                                                                   polyadenylation signal"
                                                                                                                                                                                                                                                                                  glycosylation site"
                                                                                                                                                                                                                                                                                                                                                  f in variant clone
codon"
                                                                                                                                                                                                                                                                                                                                                                                              signal peptide cleavage site"
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                                                                                                                                          Length 1475;
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                                                                                                                                                                                                                                                                                                                                                                                                                           cleavage site"
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                                                                                                                                                                                                                                                                                                                                                                  frameshift
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COMMENT
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ACCESSION
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Best Local S
Matches 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                             promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                     1497
                                                                                                                                                                                                                                                                                                                                                  sig_peptide
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                      61
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В
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ACTACTACTACTACTATAATACCCCAACCCAAC
                                actactactactactataataccccaacccaac 1531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transgenic tobacco seeds
EMBO J. 6, 3213-3221 (1987)
This sequence is a chimera between Phaseoleus vulgaris sequences
from J.L. Slightom, S.M. Sun and T.C.Hall (1983) 'Complete
nucleotide sequence of a French bean storage protein gene:
Phaseolin', Proc. Natl. Acad. Sci USA 80:1897-1901, and Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 207)
Hoffmann, L.M., Donaldson, D.D., Bookland, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays/P.vulgaris
X06175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K. Pedersen, P. Argos, S.V.L. Naravana and B.A. Larkins (1986)
'Sequence analysis and characterization of a maize gene encoding
high-sulfur zein protein of Mr 15,000',
J. Biol. Chem. 261:6279-6284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthesis and protein body deposition of maize 15-kd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phaseolin; signal peptide; zein
                                                                                                                                                                              Similarity
                                                                                                                                                         2.4%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                 /note="zein transcription initiation
161. .>207
161. .>207
                                                                                                                                                                                                                                                                              /translation="MKMVIVLVVCLALSAA" 60 c 33 g 53 t
                                                                                                                                                                                                                                                                                                                 /product="chimeric beta-phaseolin/zein"
/protein_id="CAA29542.1"
/db_xref="GI:22547"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Zea mays"
/db_xref="taxon:4577"
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beta-phaseolin/zein
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a; Poales; Poaceae; PACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Slightom,J.L., Drong,R.F., Klassy,R.C. and Hoffman,L.M. Nucleotide sequences from phaseolin cDNA clones: the major storage proteins from Phaseolus vulgaris are encoded by two unique gene
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; Fabaceae; Papilionoideae; Phaseoleae;
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signal peptide; storage protein; tandem repeat.
Phaseolus vulgaris.
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486. .488
/note="AAC (Asn) is CAC (His) in variant clones"
533
                                                                                 /note="ACGCAAGGC variant clones" 456. .464
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AYPVAIKATSWVHTGEGINANNNRNLLAGKTDNVISSIGRALDGKDVLGLTFSGSG
EEVMKLINKQSGSYFVDGHHHQQEQQKGSHQQEQQKGRKGAFVY"
87. 155
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339
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                                               ACTAGC (Thr,
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158. .159
                                                 /note="ACGCAAGGC (Thr,
ACTAGC (Thr, Ser) in va
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/db_xref="taxon:3885"
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Phaseolin nucleotide sequence diversity in Phaseolus vulgaris
Intraspecific diversity in Phaseolus vulgaris
Genome 37, 751-757 (1994)
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                                                                                                                                                                           Submitted (30-AUG-1993) James A. K. University of California at Davis,
                                                                                                                                                                                                                                                                                                                                                         Phaseolus vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cds.
                                                 /map="linkage group D7"
/clone="Sanilac 1-12"
/haplotype="'S' type beta-phaseolin"
/tissus type=""Ctyledon"
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1530
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                          /tissue_type="cotyledon"
/clone_lib="Sanilac pUC19 cDNA"
                                                                                                                  /organism="Phaseolus vulgaris"
/cultivar="Sanilac"
                                                                                                                                                            Location/Qualifiers
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            /dev_stage="cotyledonary stage"
                                                                                                   /db_xref="taxon:3885"
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726. .740
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phaseolin;
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/gene="Phs"
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/product="phaseolin"
/product="gi-403594.1"
/db_xref="gi-403594.1"
/db_xref="gi-403594.1"
/db_xref="gi-403594.1"
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swntlfkngyghirvlgrfdooskrlonledyrlvefrspeperdlriglam
swntlfkngyghirvlgrfdooskrlonledyrlvefrspeperdlriglam
ragsaaluvlvkeddrreyfflusdnpffsdhokifftflasfiqulam
pvnnpgihdfflssteaoosyloefskhileasfnskfeeinrulfeeegodegvin
pvnnpgihdfflssteaoosyloefskhileasfnstnsthuslnvllssiemkegalf
idsegikelskhaksssrslskodnyigenegalferspeperdlrigsiemegalf
vphyyskaivilvunegeahvelugpkgnketleyesyraelskddvfvipaaypvai
katsnvnftgrginannnnnnllagkfunvissigraldgkdvlgliffsgsgdevmkl
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/phenotype=".T/ type phaseolin"
/replace="qaggagggacagcaagaggagggacagcaa"
/product="phaseolin"
807. 815
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/gene="Phs"
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/product="phaseolin"
674. .679
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123. .1316
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54. .1319
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1271. .1298
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/label=27bp-repeat
/phenotype="\T' type phaseolin"
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1320. .1454
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Pred. No.
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EMBO J. 6, 3213-3221 (1987)
Location/Qualifiers
           Direct Submission Submitted (30-AUG-1993) James A. Kami, Agronomy and Range Science University of California at Davis, Davis, CA 95616, USA
                                                                                                          Kami,J.A. and Gepts,P.
Phaseolin nucleotide sequence diversity in Phaseolus.
Intraspecific diversity in Phaseolus vulgaris
                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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                                                       Kami, J.A.
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Similarity 100.0%;
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/db_xref="taxon:4577"
<1. .269
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93 c 62 g ]
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192. .197
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Matches 63; Conservative 0; Mismatches 0;
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1457. .1462
/gene="Phs"
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133. .1344
/gene="Phs"
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/gene="Phs"
61. .1347
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/gene="phs"
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1255. .1263
/gene="phs"
/function="putative glycosylation site"
1348. .1478
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/product="phaseolin"
151. .159
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/strain="G25804"
/db_xref="taxon:3884"
/clone="G25-39"
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1237. .1245
/gene="Phs"
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/function="putative
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/product="phaseolin"
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1. .1478
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/clone_lib="G25 pUC19 cDNA"
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3957
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Copyright (c) 1993 - 2000 Compugen
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		×			COLUMNIA	
Result		Query				
No.	מו	Match	Match Length DB	DB	ID	Description
1	3957	100.0	3957	22	AAS00570	Bovine phaseolin p
N	1544	39.0	1558	20	AAZ10376	Nucleotide sequenc
ω	1439	36.4	1547	20	AAX90961	Phaseolus vulgaris
4	1226	31.0	1244	20	AAZ10392	Nucleotide sequenc
₅	1173	29.6	1173	22	AAS00569	Bovine pre-pro-chy
6	887	22.4	2970	22	AAD17528	Kunitz soybean try
7	49	1.2	1098	4	AAN30063	Sequence of proren
80	49	1.2	1098	11	AAQ04683	Sequence encoding
9	49	1.2	1175	s	AAN40295	Sequence encoding

immune		24	15881		22	45	C
₽.		24	14708	0.6	22	44	a
Tumour suppressor		22	14708	٠	22	43	a
Chemically pretrea		22	14708	0.6	22	42	Ω
Chemically pretrea	AAS45352	22	6385	•	22	41	
Human immune syste		24	5376		22	40	
-	AAT89990	18	3607	•	22	39	
Human digestive sy		22	262	•	22	38	Ω
Human pancreatic c		22	262	٠	22	37	ი
		23	44242	•	23	36	
Arabidopsis thalia	AAC37875	21	1814	0.6	23	35	
Human aspartyl pro	AAS97159	24	1140	•	23	34	
Arabidopsis thalia	AAC44658	21	1083		23	3	
PCR primer used to	AAZ10389	20	25		24	32	o
Phaseolin gene pro	AAA62421	21	33	0.6	25	31	
Sequence of recomb	AAN40180	σ	1460	0.7	29	30	ი
Pre-prorennin-A ge	Þ	ω	1460	0.7	29	29	o
Rennin - casein co		12	107	0.8	32	28	
is-		20	819	0.8	33	27	
		13	186	0.8	33	26	
Sequence coding fo	״	υī	179	0.8	33	25	
DNA encoding the f		20	1096	0.9	34	24	
nisc	AAQ49459	14	637	0.9	35	23	
Sequence of prepro	Þ	4	1290		38	22	
BamHI insert from	AAN91185	10	2982	•	49	21	
=		20	2733	•	49	20	
BamHI/SalI insert		10	2727		49	19	
Sequence of recomb	AAN40180	σ	1460	•	49	18	
Pre-prorennin-A ge	AAN20043	ω	1460		49	17	
	AAN30049	4	1314	•	49	16	
uence	AAN91157	10	1291	•	49	15	
of.	AAN30022	4	1289		49	14	
Sequence of prochy	×	S	1278		49	13	
en		16	1240	1.2	49	12	
•		12	1210	1.2	49	11	
Prochymosin (prore	AA020949	13	1175	1.2	49	10	

ALIGNMENTS

RESULT AAS00570 14-MAY-2001 (first entry) AAS00570 standard; DNA; 3957 ₽P.

Bovine phaseolin promoter pre-pro-chymosin-phaseolin terminator.

Chymosin; transcription regulator; terminator sequence; soybean; corn; pre-pro-chymosin; rape seed; sunflower; cotton; tobacco; alfalfa; wheat; barley; oats; sorghum; Arabidopsis thaliana; potato; flax; linseed; rice; safflower; oil palm; ground nut; Brazil nut; coconut; castor; corlander; squash; jojoba; ds; phaseolin; promoter; terminator; mutant; French bean.

Chimeric - Bos sp: Chimeric - Phaseolus vulgaris.

promoter WO200114571-A1 terminator /*tag= b
/product= "Bovine pre-pro-chymosin"
2727...3957 /*tag= a
/note= "Phaseolin promoter"
1554..2726 Location/Qualifiers /*tag= c /note= "Phaseolin terminator"

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Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence represents a chimeric polynucleotide comprising a pre-pro-chymosin, a phaseolin promoter and a phaseolin terminator. Chymosin can be produced in a plant seed through introduction of a chimeric nucleic acid molecule, comprising a nucleic acid sequence encoding a chymosin polypeptide operatively linked to transcription regulator and terminator sequences, into a plant cell. The sequences are useful for producing plant seeds, in particular seeds of soybean, rape seed, sunflower, cotton, corn, tobacco, alfalfa, wheat, barley, oats, sorghum, Arabidopsis thaliana, potato, flax/linseed, safflower, oil pal groundnut, Brazil nut, coconut, castor, coriander, squash, jojoba and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing chymosin in seeds of
transforming plant cell with a
linked to transcription regular
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Local Similarity 100.
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Matches 1226; Conservative
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Modifying ng fatty acid metabolism and producing specific p n in plants, polymers in useful seeds for increasing

English.

CC is used to construct plasmids for the expression of the P. putida CC faoAB gene. The gene encodes an enzyme that may be used in the CC manipulating the metabolism of a plant, and comprises expressing a CC heterologous gene encoding fatty acid oxidation enzymes in the CC cytosol or plastids other than the peroxisomes, glyoxisomes or CC mitochondria of the plant. The method may be used to enhance the CC biological production of polyhydroxyalkanoates or novel oil compositions of a compounds in this way include Brassicas, maize, soybean, cottonseed, CC sunflower, palm, coconut, safflower, peanut, mustards, flax, tobacco and CC alfalfa. The method may also be used to production and therefore increase the production of biomass (leaves, Stalks) by plants.

Sequence 1244 BP; 456 A; 174 Ç 178 G; 436 T; 0 other;

31.0%;

0;

Score 1226; D Pred. No. 0; 0; Mismatches

DB

20;

Length

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Indels

0;

Gaps

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                                                                                                                                                                 Chymosin; transcription regulator; terminator sequence; soybean; corn; pre-pro-chymosin; rape seed; sunflower; cotton; tobacco; alfalfa; wheat; barley; oats; sorghum; Arabidopsis thaliana; potato; flax; linseed; rice; safflower; oil palm; ground nut; Brazil nut; coconut; castor; corlander; squash; jojoba; ds.
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Matches 1173
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tccaacattgtggacattcaacagacagtaggacttagcacccaagaaccaggtgatgtc
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RESULT
AAD1752
ID 7828
ID 7828
ID 7828
ID 782
IO-IO-IO-IO
DT 10-IO-IO
DT 10-IO
DT 8094
KW SO94
KW SO94
KW S128
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The patent discloses hypoallergenic transgenic soybeans and recombinant cc expression constructs to lower soybean vacuolar protein, commonly known cc as p34 (Gly m Bd 30K or Gly m 1) and other allergens such as Gly m IA, cc Gly m IB, rGLY m3 or Glycinin Gl (alaBlb). The allergen content of the cc Soybean is reduced by sense suppression which is accomplished by using the expression construct that comprises a nucleic acid fragment encoding the allergen. The constructs are useful for producing hypoallergenic ct transgenic soybean plants which can be used to make hypoallergenic cc soybean products which can be used to make hypoallergenic cformulas) and animal feed applications. The oil made from seeds of the hypoallergenic transgenic soybean plants can be used as ingredients, cc as coatings, as salad oils, as spraying oils, as roasting oils, and cc and snack foods, confectionery products, syrups and toppings, sauces, batter and breading mixtures, baking mixes and doughs. The present cc sequence is a DNA encoding kunitz soybean trypsin inhibitor (KSTI cc or KTi3), a minor soybean seed allergen.
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                      The inventors claim recombinant plasmids contg. the cDNA of calf prorennin. Specified plasmids are pCR 10001 and pCR2001 (contg. the whole sequence plus the lac promoter region). Also new are microorganisms transformed with the plasmids, esp. E. coli CR1 (ATCC
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DB; AAP30603.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tataatataacatttatctataaaaaagtaaatattgtcataaatctatacaatcgttta
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                                                                                                                                                                                                                                                                                                                                                                                                                                    gccttgctggacgactctcaattatttaaacgagagtaaacatatttgactttttggtta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atttaatttattgcttcttacagataaaaaaaaattatgagttggtttgataaaatat
                contg. plasmid pCR2001.
                                                                                                                                                          BEPPU
                                                                    Page
                                                                                                                                         Uozumi T,
                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                     20-23;
                                                                                                                                                                                                                                                                                                   enzyme;
                                                                                                                                                                            81JP-0131631
                                                                                                                                                                                            82EP-0107601
                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         cDNA;
                                                                                            pro:rennin
                                                                   32pp;
                                                                                                                                         Nishimori
                                                                                                                                                                                                                                                                                                                    cDNA in
                                                                                                                                                                                                                                                                                                   protease; ss
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                                                                    English.
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                                                                                              DNA -
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Sequence 1098

BP;

252 A;

326

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301 <u>ن</u>

219

ij 0 other;

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RESULT AAQUAGES AAQUAGES AAQUAGES AAQUAGES AAQUAGES AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AAQUA AA
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AAN40295
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Best Local S
Matches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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plasmid
                   Key
sig_peptide
                                                                                                                Cheese-making;
                                                                                                                                                     Sequence encoding a polypeptide displaying
                                                                                                                                                                                                                                                                   AAN40295
                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2209
                                                                              Bos taurus
                                                                                                                                                                                            04-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complex plasmid and microbe - contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1990-168358/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-APR-1990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ04683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ04683 standard; DNA; 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BEPP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        581 tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity hes 49; Conserv
                                                                                                                                                                                                                                                                                                         9
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49; Conserv
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                                                                                                                                                                                                                                                                   standard; mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1098 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
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ilarity 100.0%;
Conservative
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Llarity 100.0%;
Conservative
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                                                                                                                                                                                         (first entry)
                                                                                                                  recombinant protein; rennet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88JP-0302176
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Location/Qualifiers
21..69
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                   BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; I
1.5e-11;
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                                                                                                                  substitute;
                                                                                                                                                   milk clotting activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Τ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                  milk clot; ss
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                                                                                                                                                                                                                                                                               RESULT
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Best Local Similarity 75.5%;
Matches 37; Conservative
28-OCT-1988;
11-MAY-1984;
12-DEC-1986;
31-MAR-1983;
28-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                       Also claimed is E.coli JM83/pLC7 (ATCC 39325) which is transformed with pLC7 contg. the prorennin derived sequence fused in phase wit B-galactosidase. The pLC7 prorennin expression plasmid includes sequences which code for both the pseudorennin and mature rennin cleavage sites between AAs 28-29 and AAs 42-43, respectively.
                                                                                                                                                                                                                                                                                                       Cashion LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-1984.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAP40559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1984-277277/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CODO-) CODON GENETIC ENG
                                                                                                                                                               Bos
                                                                                                                                                                                                       Prochymosin (prorennin) gene from calf.
                                                                                                                                                                                                                                             AAQ20949;
                                                                                                                                                                                                                                                              AAQ20949 standard; cDNA; 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressed in transformed bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant DNA coding for milk clotting
                                                     28-OCT-1988;
                                                                       21-JAN-1992
                                                                                         US5082775-A
                                                                                                                                                                               clotting
                                                                                                                                                                                                                            13-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1175 BP; 263 A; 355 C; 319 G;
                                                                                                                                                                                                                                                                                10
                                                                                                                                                               taurus.
                                                                                                                                                                                         zymogen; autocatalytic
                                                                                                                                                                                activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McCaman MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                           (first entry)
88US-0263927.
84US-0609495.
86US-0940199.
83US-0480860.
86US-0856700.
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/*tag= l
                                                      88US-0263927
                                                                                                         /product=
/note= "al
                                                                                                                                    Location/Qualifiers 21..1158
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                                                                                                         "also known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice
                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                            Score 49; DB
Pred. No. 1.4e
l2; Mismatches
                                                                                                                                                                                                                                                              ВP
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                                                                                                                                                                                         activation;
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                                                                                                         prochymosin"
                                                                                                                                                                                                                                                                                                                                                                                        238 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide - which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SR;
                                                                                                                                                                                         pseudorennin;
                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                             Length 1175;
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                                                                                                                                                                                          milk;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The prorennin (prochymosin) sequence was obtd.from mRNA from unweaned calf's stomach (abomasum). To identify rennin-specific mRNA species, hybridisation with rennin specific probes was performed using probes derived from the published amino acid sequence of prorennin (Foltmann et al., J. Biol. Chem. 254, 8447-8456 (1979)) (see AAQ23391, 2). Reverse transcriptase was used to transcribe mRNA to account the published was used to transcribe mRNA to account the published was used to transcribe mRNA to account the published was used to transcribe mRNA to account the published was used to transcribe mRNA to account the published was used to transcribe mRNA to account the published was used to transcribe mRNA to account the published was used to transcribe mRNA to account the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the published was the publish
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rennin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1175
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                                                                   Hartl P,
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11-APR-1990;
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Pred. No. 1.4e-11;
.2; Mismatches 0
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Best Local
The DNA is that of a mammalian gene (open reading frame) encoding chymosin. The gene was placed in operable linkage with the al-3 promoter (see AATO3005). The al-3 gene controls the production of geranyl geranyl pyrophosphatase (GGPP) synthetase. GGPP is a precursor for carotenoids and xanthophylls. It has been shown that exposure to light increases the transcription level of GGPP synthetase 15-45 fold. Light activates a number of genes in the common bread mould, Neurospora. This can be used to regulate the expression of genes encoding heterlogous proteins, e.g. chymosin, in recombinant production systems. Use of a light-regulated promoter is a simple and effective way to control expression and allows timing to be adapted to the physiological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha-S1-casein gene in the prodn. of DNA constructs. The heterologous peptide/protein together with parts of the peptide or protein may also be human insulin-like growth factor I. The constructs provide high yields of the protein with simple recovery from the milk. Activation of the gene occurs only in the mammary gland. See also AAQ14050, AAQ14774-77.
                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid for expression of heterologous protein - contains albino promoter for light induced expression in filamentous fu
                                                                                                                                                                                                                                                                                                                                                                         albino
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                                                                                                                                                                                                                                                                                                                      Example
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                                                                                                                                                                                                                                                                                                                   Fig 7; 26pp; English.
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gene; expression; control; chymosin; ss.
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Query Match Best Local Matches

Similarity

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Best Local
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                            The inventors claim the prochymosin gene comprising a nucleotide sequence from (a) the 1st codon (GCT) to the 365th codon (ATC), or (b) the 5th codon (CGG) to the 365th codon (ATC); and recombinant plasmids harboured by Escherichia coli strains deposited as FERM BP-262, -263 and -264. Any portion of the nucleotide sequence as described in AAN40055 can be used. Also claimed is a vector derived from plasmid pBR322. Typically plasmid pCR501 is obtd. from pCCT 2. The transcriptional direction of pCCT 3 is opposite to that of pCCT 2; it is clockwise in pCCT 2 (5' to 3') whereas counter
Sequence 1278 BP;
                                                                                                                                       Disclosure; Fig 1; 59pp;
                                                                                                                                                           Expression plasmid comprising prochymosin gene and vector - useful for transforming Escherichia coli for prochymosin pr
                                                                                                                                                                                                                                                                                   09-MAR-1983;
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                                                                                                                                                                                                                                                            (BEPP/) BEPPU T.
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49; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                274 A;
                                                                                                                                                                                                                                        Nishimori
A;
                                                                                                                                         English.
384 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49;
Pred. No.
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 326
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                                                                                                                                                                                                                                       Shimizu
G;
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1.4e-11;
0;
 259
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Τ;
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0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 other;
                                                                                                                                                                                                                                      Kawaguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1240;
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RESULT 15
AAN91157
ID AAN911
XX
AC AAN911
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DT 07-JUN
XX
Cloned
XX
KW Lactic
KW protei
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AAN30022
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                                                                                                                                                            망
                                                                                                                                                                                                      Query Match 1.2%; Sometimes 1.2%; Sometimes 100.0%; Matches 49; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAN30022
                                                                                                                                                         The inventors claim isolated chymosin (rennin) and prochymosin genes from calves, and plasmids contg. the genes which are capable of replicating in a prokaryotic organism. The prokaryotic organism is pref. an Escherichia species, esp. E. coli p Gx 1225 (NRRL B-15061). The microorganisms transformed by the plasmid are also claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microbial vector; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protolytic enzyme; zymogen; rennin; chymosin; cheese making;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-1992
Lactic acid bacteria; proteinase; pSK112; s:
                                                                                                                                                                                                                                                                                                                                                                         Isolated chymosin or rennin and prochymosin genes - which replicate in prokaryotic organisms, esp. Esche and organisms used for chymosin biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1983-820813/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-NOV-1983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         613
                                  Cloned sequence of (pro)chymosin.
                                                         07-JUN-1990
                                                                                                    AAN91157 standard; DNA; 1291 BP.
                                                                                                                                                                                                                                                             Sequence 1289 BP; 310 A; 391 C;
                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 33-36; 43pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENEX CORP.
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                                                        (first entry)
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82US-0394433
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1..1140
/*tag= a
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            cheese; Streptococcus cremoris
                                                                                                                                                                                                      Score 49; DB 4; L
Pred. No. 1.4e-11;
0; Mismatches 0;
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                                                                                                                                                                                                                                                              327 G;
                                                                                                                                                                                                                                                              260 T; 1 other;
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Escherichia coli,
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            SK112; chymosin;
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B
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Best Local Similarity
Matches 49; Conserva
                                                                                                                                                                            The DNA encoding prochymosin can be cloned into a plasmid (esp. from S. cremoris SK112) and used to produce large amts of the protein by recombinant DNA techniques. This could overcome the shortage of prochymosin due to shortage of calf stomachs and increasing cheese prodn. Prochymosin is also used in prodn. of yoghurt, butter and buttermilk. See also AAN91158-N91160.
                                            DNA fragment having region specific for lactic acid bacteria is contained in plasmid in microorganism used in prodn. of protein and food prodn. eg cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 precursor_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                        Sequence 1291 BP; 323 A; 385 C; 326 G; 257 T; 0 other;
                                                                                                                                                                                                                                                                  Disclosure; fig 2; 43pp; Dutch.
                                                                                                                                                                                                                                                                                                                                         WPI; 1989-030097/04.
P-PSDB; AAP94144.
                                                                                                                                                                                                                                                                                                                                                                                                   (NEZU-) NEDERL INS ZUIVELON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-1987;
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                                                                                               Conservative
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                                                                                          1.2%; but
100.0%; Pr
100.0%; 0;
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2002, 01:58:17
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Pred. No. 1.4e-11;
0; Mismatches 0;
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Search completed: August 1, 2002, 01:58:17 Job time: 16992 sec

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2000 Compugen Ltd.
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702 727 782	136 214 312 442 500 560	383 430 472 399 240 468 660	Length
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BG872501 BH522720 BG432457	BE763309 C25503 AU053870 AAA41444 AU052887 BH366372 BH366372	BG938086 BG937697 BG9378320 BG937723 BG937723 AG073125 AA394733 AG091550	SUMMARIES
BG872501 602793535 BH522720 BOHGT42TR BG432457 602495493	BE763309 RC1-NT003 C25503 C25503 Dict AU053870 AU053870 AA441444 LD16384.5 AU052887 AU052887 BH366372 CH230-204 AQ635511 RPCI-11-4	BG938086 1Abo11A08 BG937697 1Abo05E01 BG938320 1Abo15E12 BG938723 1Abo05D06 AU073125 AU073125 AA394733 26530 Lam	Description

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AV439574	AV542531	AV532027	AZ457432	AV555646	AZ107068	AV557282	AV548208	AV518638	AI479358	AV536021	AQ711285	AA411566	AV559941	AV518232	AQ192651	AA411567	AA969042	AV538262	T20903	AV532492	вн261085	AQ907383	BB489847	BB493759	AU073299	BI974502	
		AV532027	AZ457432	AV555646	AZ107068	AV557282				AV536021	AQ711285	AA411566	AV559941		\vdash	AA411567	AA969042	AV538262	T20903 2	AV532492 AV532492	вн261085	ω	BB489847	вв493759	AU073299	BI974502	
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL RESULT BG938086 LOCUS COMMENT FEATURES DEFINITION source Beef Genomics Laboratory Dept of AFNS, University of Alberta 410 Agri/For, Dept of AFNS, U of A, Tel: 780 492 0169 Fax: 780 492 4265 Email: smoore@afns.ualberta.ca 1 (bases 1 to 383) Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G. cDNA's from bovine abomasum tissue Unpublished (2001) Contact: Dr. Stephen Moore BG938086 BG938086.1 GI:14337458 EST. BACKWARD: M13 Reverse Seq primer: T3 primer High quality sequence stop: POLYA-NO. The sequence best matches gb:BPU19786 (Bos primigenius prochymosin mRNA, complete cds) in main database at high score of 735.0 and E-value of 0.0 PCR PRimers Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bos taurus sequence. BG938086 383 bp mRNA linear EST 11-JUN-2001 1Abolla08 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA FORWARD: M13 Forward Bovidae; Bovinae; Bos. /organism="Bos taurus" /db_xref="taxon:9913" /clone_lib="Bovine Abomasum cDNA Library" /clone_smales and one female mixed" /tissue_type="Gastrointestinal tissue (GIT)" Location/Qualifiers Edmonton, AΒ, T6G 2P5, Canada

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RESULT
BG937697
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ORIGIN
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AUTHORS
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KEYWORDS
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 52
TGTTCTCGGTTTACATGGACAGGAATGGCCAGGAGAGCATGCTCACGCT 106
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BG937697.1
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1Abo05E01
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49; Conserv
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Moore, S.S., Hansen, C., Li, C., cDNA's from bovine abomasum ti Unpublished (2001)
Contact: Dr. Stephen Moore
                                                      49; Conserv
                                                                                                                                                                                                                                                                                                                                   Seq primer: T3 primer 
High quality sequence
                                                                                                                                                                                                                                                                                                                                                                                      The sequence best matches gb:BOVCHYMOA mrna)in main database at high score of PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                           Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COW.
                                                                                                                                                                                                                                                                                                                                                             BACKWARD: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                               Email: smoore@afns.ualberta.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
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                                                                                                                                                                                                                                                                                                                                  quality sequence stop:
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/lab_host="XLI-BlueMRF'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"
a 111 c 113 g 76 t
                                                                                                                                     /dev_stage="Young adult"
/lab_host="Xil-BlueWRE'-strain"
/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
130 c 119 g 84 t
                                                                                                                                                                                                      /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="Bovine Abomasum cDNA Library"
/csxx="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Bovine Abomasum cDNA Library
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3. 2.5e-08;
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2.7e-08;
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taurus
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5', mRNA
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VERSION
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DEFINITION
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                                                                                        sequence.
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1Abo15E12
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49; Conserv
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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Contact: Dr. Stephen Moore
                                                                                                                                                     BG937723 399 bp mRN/
1Abo05D06 Bovine Abomasum cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVCHYMOA (bovine chymosin a (rennin)
mrna) in main database at high score of 928.0 and E-value of 0.0
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec Bovidae; Bovinae; Bos.
1 (bases 1 to 399)
                                                           Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: T3 primer High quality sequence stop:
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                                                                                                                                                                                                                                                                                                                                                                                                         104
                                                                                                                                                                                                                                                                                                           1.2%; Scilarity 100.0%; F
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="Young adult"
/lab_host="XII-BlueMRF'-strain"
/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
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Bovine Abomasum cDNA Library
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Pred. No.
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2.4e-08;
thes 0;
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                              Pecora;
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CDNA 5', mRNA
                                              Euteleostomi;
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                                 Bovoidea;
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                                                                                                                                                                                     Developmental cDNA in Dictyostelium discoideum (1999)
Unpublished (1999)
Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                              AU073125 240 bp mRNA linear EST 24-JUN-199 AU073125 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSG202, mRNA sequence.
AU073125 AU073125.1 GI:5179546
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410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                       Urushihara, H.
                                                                                                                                                                                                                                                    Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 240)
                                                                                                                                                                                                                                                                                   Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: smoore@afns.ualberta.ca
The sequence best matches gb:BPU19786 (Bos primigenius prochymosin mRNA, complete cds)in main database at high score of 767.0 and E-value of 0.0
                                                                                                                                                      University of Tsukuba
                                                                                                                                                                                                                                                                                                  Dictyostelium discoideum.
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Seq primer: T3 primer
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llarity 100.0%;
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                                                                                                          Ten-nodai, Tsukuba, Ibaraki 305, Japan
d402hu@sakura.cc.tsukuba.ac.jp
T = Dictyostelium discoideum cDNA proje
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             /organism="Dictyostelium
/strain="AX4"
/db_xref="taxon:44689"
/clone="$SG202"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Young adult"
/lab_host="XL1-BlueMRF'.strain"
/lab_host="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
 /clone_lib-"Dictyostelium discoideum SS
                                                                                           Location/Qualifiers
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/cell_type="Epithelial"
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/sex="Two males and one female mixed"
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                                                                                                          cDNA project in
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 (H.Urushihara)"
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AA394733.1
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                    . Similarity
25; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lansing, Mi
Tel: 517-353-0854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant Physiol. 106, 1241-1255 (1994)
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Seq primer: M13 -21 dye primer
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MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 517-353-9168
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                                                                 0.6%; S
llarity 100.0%;
Conservative 0;
                                                                                                                                                                                                   //Clone_lib="Lambda-PRL2"
//Clone_lib="Lambda-PRL2"
//note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_2: Not;
/note="Vector: lambda Zip-Lox; The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed CDNA."

//Clone=lib="Lambda-PRL2"
//Clone=lib="Lambda-PRL2"
//Clone=lib="Lissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed CDNA."

//Clone=lib="Lambda-PRL2"
//Clone=lib="Lissue Cloned with Sal-Not arms using oligo dT primed CDNA."
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/strain="var columbia"
/db_xref="taxon:3702"
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                                                                 Score 25; DB
Pred. No. 45;
0; Mismatches
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                                                     AUTHORS
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AG091550
AG091550 1 GI:16643352
GSS; GSS (genome survey seques of troglodytes male lymphologytes male lymphologytes male lymphologytes male lymphologytes male lymphologytes male lymphologytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-AUG-2001) Asao Fujiyama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fujiyama,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fujiyama, A., Hattori, M.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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1 (bases 1 to 136)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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RC1-NT0033-090800-016-a01 NT0033
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R.Site 2
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/clone_lib="PTB Chimpanzee Male
/166 c 130 g 236 t
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/db_xref="taxon:9598"
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gutheria; Primates; Catarrhini; Hominidae;
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36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence tags
Proc. Natl. A
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Seq primer: puc 18 forward
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                                                                                                                                                                                        Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y. The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage o
                                                                                                                                                                                                                                                                                                                                                                                                                                                     C25503 Dictyostelium discoideum SL discoideum cDNA clone SLA138, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.ludwig.org.br/scripts/gethtml2.pl?ti-&t2=RC1-NT0033-090
                                      Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten nodai, Tsukuba, Ibaraki 305, Japan
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99156227
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                                                                                                         Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                 Morio,T., Urushihara,H.,
                                                                                                                                                                                                                                                                                                                          Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
PROJECT =
                      Email: d402hu@sakura.cc.tsukuba.ac.jp
                                                                                                                                                                                                                                                                                                 (bases 1 to 214)
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Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="Adult"
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/db_xref="taxon:9606"
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'Dictyostelium discoideum
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(H.Urushihara) Dictyostelium
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AA441444
LD16384.5prime LD Drosophila
Drosophila melanogaster cDNA
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                                                                                                                                                                                                                                                                                                                                                                                     University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Hideko Urushihara
Institute of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M
Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H.,
Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.
Developmental cDNA in Dictyostelium discoideum
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                             d402hu@sakura.cc.tsukuba.ac.
T = Dictyostelium discoideum
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                                                                                                                                                                                                                                /clone_lib="Dictyostelium discoideum SL (H.Urushihara)"
/dev_stage="slug"
50 c 50 g 102 t
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/Strain="AX4"
/db_xref="taxon:44689"
/clone="SLA138"
/clone="blictyostelium discoideum
/dev_stage="8.lug"
_ 28 g 72 t
                                                                                                                                                                                                                                                                            /db_xref="taxon:44689"
/clone="SLJ838"
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/strain="AX4"
                                                                                                                                                                                                                                                                                                                                                 Cocation/Qualifiers
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bp mRNA linear EST 19-APR-2001
melanogaster embryo BlueScript
clone LD16384 5prime, mRNA sequence.
                                                                                                                                                DB 9; 1.3. 1.4e+02; 0;
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1.7e+02;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 442)
Harvey_D., Brokstein, P., Hong,L., Evans-Holm,M., Su,C., Tsang
                                                               3-3-10 Ten-nodai, Tsukuba, Ibaraki 305,
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA
                                                                                                                                                                                                                                                     Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yos
Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasuka
Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
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500 bp mRNA linear EST 28-APR-19-
AU052887 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
discoideum cDNA clone SLF272, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                          Dictyostelium discoideum. Dictyostelium discoideum
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High quality sequence stop: 254.
Location/Qualifiers
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BDGP/HMI Drosophila EST Project
Unpublished (2001)
On Jun 2, 1997 this sequence ver
                                                                                                                                        University of Tsukuba
                                                                                                                                                              Institute of Biological Sciences
                                                                                                                                                                                    Contact: Hideko Urushihara
                                                                                                                                                                                                              Unpublished (1998)
                                                                                                                                                                                                                                    Developmental cDNA in Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                              Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
1 (bases 1 to 500)
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Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
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/organism="Dictyostelium discoideum"
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/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Drosophila melanogaster"
/db_xref="BDGP_EST:BDcln015599"
/db_xref="taxon:7227"
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1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., (Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (199)
Other_GSSs: CH230-204G22.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BH366372.1 GI:17297106 GSS.
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   24;
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                                                                                                                                                                                                                                                                                                                                                    (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html plate: 204 row: G column: 22
                                                                                                                                                                                                                                                                                                                                                                                                     Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/Dacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Norway rat.
                                                                                                                                                                                                                                                                                                                       Class: BAC ends
                                                                                                                                                                                                                                                                                                                                     Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: szhao@tigr.org
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0.6%;
ilarity 100.0%;
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/db_xref="taxon:44689"
/db_one="SLF272"
/clone_lib="Dictyostelium discoideum SL (H.Urushihara)"
/dev_stage="slug"
/dev_stage="slug"
88 c 83 g 160 t
                                                                                                   Pieter de Jong"
1 103 c 89
                                                                                                                                    /note="Vector: pTARBAC2.1; Site_1: ECORI; Site_2: ECORI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                      /strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                   /cell_type="Brain"
                                                                                                                                                                                      /sex="Female"
                                                                                                                                                                                                    /clone_lib="CHORI-230 Segment 1"
                                                                                                                                                                                                                  /clone="CH230-204G22"
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pred. No. 98;
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Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.seg primer: T?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Contact: Shaying 2
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,J.C.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RPCIII Human Male BAC Library"
135 c 146 g 171 t
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AUTHORS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 702)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM/10848 row: column: 09

High quality sequence stop: 655.

Location/Qualifiers

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/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1: Not1: Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT. Average insert size 13 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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/strain="FVB/N"
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